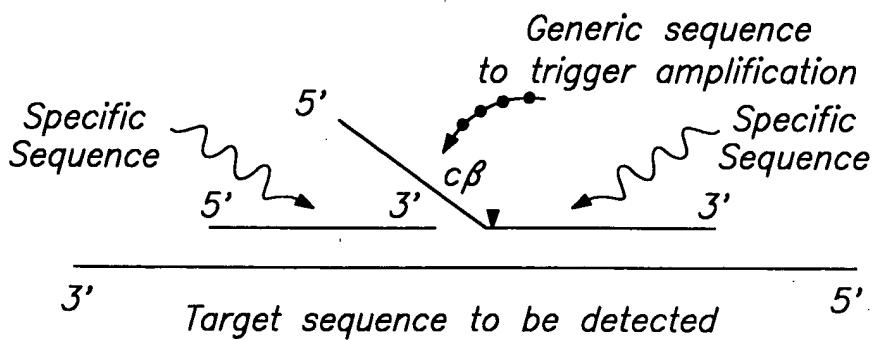
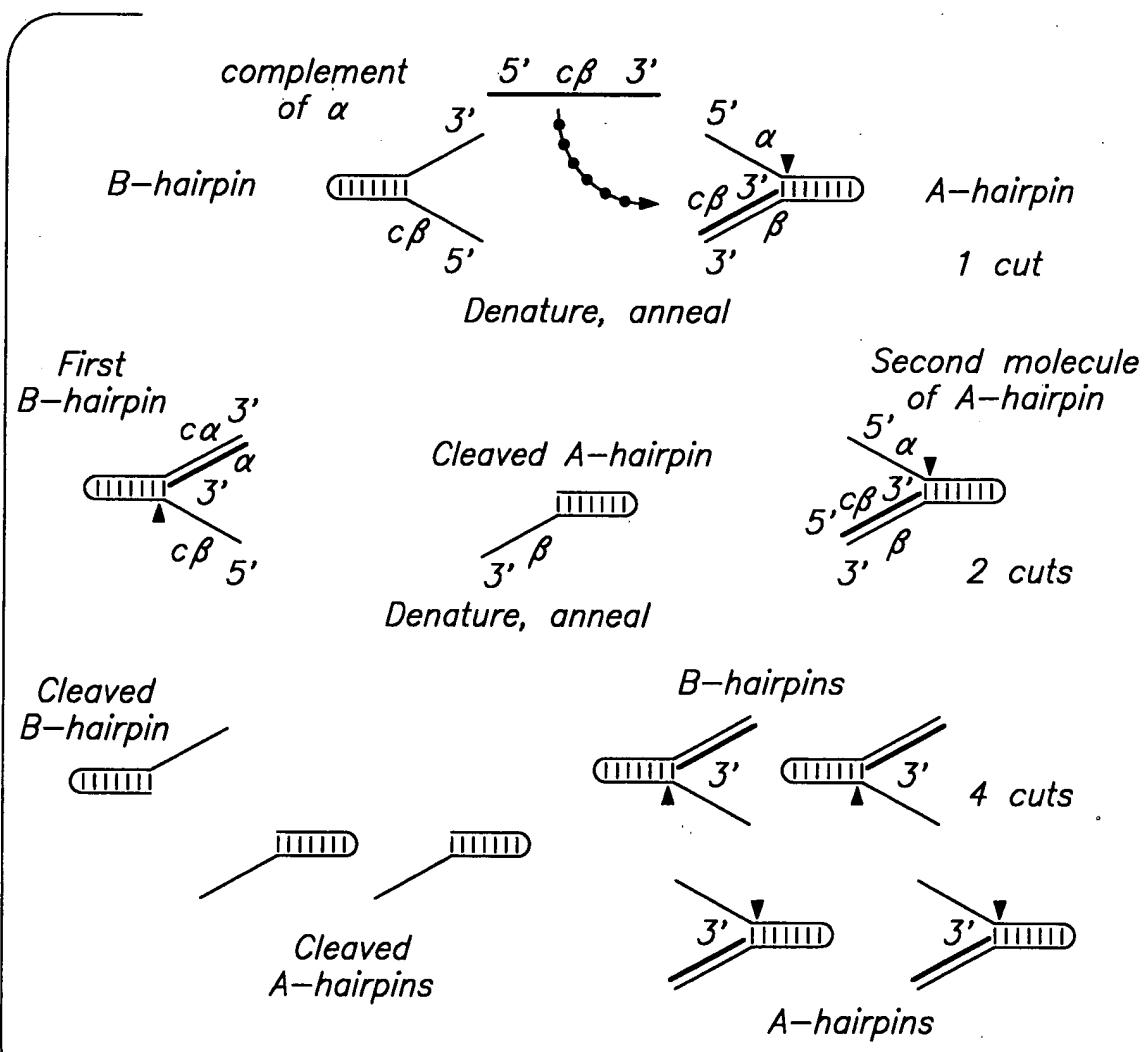


FIG. 1A

**FIG. 1B**



**PART ONE: TRIGGER REACTION**



**PART TWO: DETECTION REACTION** —

FIG. 2A

FIG. 2B

MAJORITY	[SEQ ID NO:7]	CGAGGGGAGGAGCTXGTGCCACCTGGCAAAGGGAAAGGAGGGTACGGAGCTGGCATCCTC
DNAPTAQ	[SEQ ID NO:1]	C.....G.....G.....G.....C.....C.....C.....C..... 417
DNAPTFL	[SEQ ID NO:2]	T.....G.....G.....G.....G.....G.....G.....G..... 414
DNAPTR	[SEQ ID NO:3]	T.....G.....G.....G.....G.....G.....G.....G..... 420
MAJORITY		ACGGGGACCCGACCTCTACGACCTCTCCGACCCATGGCGCTCCACCGAGGGTACCTCA
DNAPTAQ		.....AAA.....T.....G.....G.....GA.....A.....T.....G..... 487
DNAPTFL		.....T.....A.....G.....C.....G.....A.....T.....G..... 484
DNAPTR		.....A.....G.....C.....G.....A.....G.....G.....G..... 490
MAJORITY		TGACCCGGCTGGCTTGGAGAAGTACGGCTGAGGCCGTGGTGGACTACGGCCCTGG
DNAPTAQ		.....G.....A.....A.....G.....G.....G.....G.....G..... 557
DNAPTFL		.....A.....AC.....C.....C.....C.....A..... 554
DNAPTR		.....A.....C.....G.....T.....C.....C.....T..... 560
MAJORITY		GGGGACCCCTGGACACCTCCCCGGCTAAGGGATCGGGAGAACACCCCCXGAAGCTCGTCA
DNAPTAQ	C.....GAG.....T.....G.....G.....G.....G.....A..... 627	
DNAPTFL	.....G.....T.....A.....G.....G.....A.....G.....A..... 624	
DNAPTR	.....A.....T.....G.....A.....T.....A..... 630	
MAJORITY		GAGTGGGGAGCTGGAAACCTCTCAAGAACCTGGACCCGTGAAGCCCG.....CTTCCGGAGAACA
DNAPTAQ		.....GG.....G.....A.....A.....A.....A.....A..... 694
DNAPTFL		.....T.....G.....G.....A.....T.....T.....G.....G..... 691
DNAPTR		.....A.....A.....A.....A.....A.....A.....A..... 700

**FIG. 2C**

MAJORITY	[SEQ ID NO:7]	TCCAGCCCCAGATGGAXGACCTGAXGCTCTCTGGAGCTTCCAGGAGCCGGACCTGGCCCTGGA	
DNAPTAQ	[SEQ ID NO:13]	.....T.....C.....T.....A.....C.....GG.....A.....	764
DNAPFL	[SEQ ID NO:2]	.....GG.....G.....C.....GG.....T.....C.....A.....T.....A.....T.....	761
DNAPTR	[SEQ ID NO:3]	.....A.....C.....A.....G.....G.....T.....C.....G.....G.....	770
MAJORITY		GGTGGACTTCCGCCAACGXGGGGAGCCGGAGGGCTTACGGCTTCTGGAGACCTGGACTT	
DNAPTAQ		.....AA.....AA.....A.....T.....A.....T.....T.....T.....	834
DNAPFL		.....GG.....G.....C.....C.....GACCA.....A.....T.....T.....GC.....T.....T.....	831
DNAPTR		.....C.....C.....C.....C.....C.....C.....C.....C.....C.....	840
MAJORITY		GGCACCTCTCCACGAGTTGGCCTCTGGAGGGCCCAAGGCCCTGGAGGCCCCCTGGCCCCCG	
DNAPTAQ		.....T.....AA.....A.....A.....G.....G.....GGCA.....	904
DNAPFL		.....A.....A.....A.....G.....G.....GGCA.....	901
DNAPTR		.....C.....C.....C.....C.....C.....C.....C.....C.....	910
MAJORITY		CGGAACGGCTTCTGGCTTCTGGCTTCTGGGGGGAGCCATGCCCCAGCTTCTGGCTTGGC	
DNAPTAQ		.....A.....A.....A.....A.....A.....A.....A.....A.....	974
DNAPFL		.....T.....T.....T.....T.....T.....T.....T.....T.....	971
DNAPTR		.....C.....C.....C.....C.....C.....C.....C.....AAA.....	980
MAJORITY		GGGGCCAGGGAGGGCTTCAAGGGAGGGACACCTTAXGGCTXAGGGACTXAGGAGGTC	
DNAPTAQ		.....G.....C.....C.....C.....T.....A.....AA.....C.....G.....C.....	1044
DNAPFL		.....T.....GG.....G.....C.....C.....T.....A.....G.....G.....G.....	1041
DNAPTR		.....T.....G.....C.....C.....G.....G.....G.....GGC.....G.....A.....A.....G.....C.....	1050

## FIG. 2D

"Replacement Sheet"

MAJORITY	CCCGCATGGCTCCCTACCTCCGGACCCCTCCAAACACCAACCCCCGAGGGGTGGCGGGGCTACGG	
DNAPTAG	[SEQ ID NO:1] ..... G. T. ..... A. ..... AG. ..... C. ..... A. ..... T. G. ..... CC. ..... C. ..... C. ..... 1114	
DNAPFL	[SEQ ID NO:2] ..... AA. ..... G. ..... G. ..... C. ..... G. ..... T. G. ..... A. A. ..... T. G. ..... 1111	
DNAPTR	[SEQ ID NO:3] ..... C. ..... C. ..... C. ..... C. ..... T. C. ..... G. A. ..... G. ..... G. ..... 1120	
MAJORITY	GGGGGACTGGACGGAGGAXGGGGGAGGGGCGCTCCGAGAGGCTTCCXGAACCTXXXGGAC	
DNAPTAG	C. ..... G. ..... G. ..... GC. ..... T. ..... GC. ..... GGC. ..... GTG. ..... G. ..... 1254	
DNAPFL	..... T. ..... A. ..... GG. ..... C. C. ..... A. C. ..... AAA. ..... 1251	
DNAPTR	..... G. ..... G. GGC. G. ..... G. G. ..... CAT. G. ..... CCTA. ..... 1260	
MAJORITY	CGCCTTGGGGGAGGAGGGCTTGGCTTACCAAGAGGTGGAGAACCCCTTGGGGGTGCTGG	
DNAPTAG	A. G. ..... A. ..... A. ..... A. ..... AC. C. ..... G. ..... G. ..... GCT. ..... GCT. ..... 1324	
DNAPFL	..... A. ..... A. ..... A. ..... G. ..... G. ..... G. ..... G. ..... GT. ..... 1321	
DNAPTR	..... G. ..... A. ..... A. ..... C. ..... C. ..... A. ..... C. ..... 1330	
MAJORITY	CCGACATGGAGGGCAGGGGTGGGCTGGACGTGGCTACCTCCAGCCCTXCCCTGGAGGTGGCGGA	
DNAPTAG	..... G. ..... C. ..... T. ..... AG. ..... T. G. ..... G. ..... G. ..... 1394	
DNAPFL	..... GG. ..... G. ..... G. ..... G. ..... G. ..... A. C. ..... 1391	
DNAPTR	..... G. ..... A. ..... T. ..... T. ..... G. T. ..... 1400	

FIG. 2E

MAJORITY	GGAGATCCCCCTGGAGGAGCTTCCCCCTGGGGACCCCTGAACTCAACTGGGGAC	
DNAPTAQ	[SEQ ID NO:1] .....	1464
DNAPTFI	[SEQ ID NO:2] .....	1461
DNAPTR	[SEQ ID NO:3] .....	1470
MAJORITY	CAGCTGAAAGGCTCTTACGGAGCTXGGCTTCCCCCATGGCAAGAGACAGACXGGAAAC	
DNAPTAQ	..... C..... A..... C..... A..... C..... 1534	
DNAPTFI	..... G..... G..... G..... G..... G..... A..... 1531	
DNAPTR	..... T..... T..... T..... T..... G..... C..... A..... 1540	
MAJORITY	GCTCCACGCCCCCTGCTGGAGCCCTXGGXGAGCCACCCATCTGAGAAGATCTGACTA	
DNAPTAQ	..... C..... C..... C..... C..... C..... 1604	
DNAPTFI	..... T..... G..... A..... G..... GGGC..... 1601	
DNAPTR	..... G..... A..... G..... C..... C..... 1610	
MAJORITY	GGGGACCTACCAAGCTCAAGAACACCTACATXACCCCTGCCXGCTCGTCCACCCGAGGAGGGC	
DNAPTAQ	..... G..... G..... T..... T..... G..... A..... A..... 1674	
DNAPTFI	..... A..... A..... C..... C..... G..... A..... C..... 1671	
DNAPTR	..... G..... G..... G..... AAG..... G..... G..... 1680	
MAJORITY	CGCTCCACACCCCTCAACCAAGACGGCACGGCAGGCTTAGCTCCACCCAACTGC	
DNAPTAQ	..... A..... T..... C..... 1744	
DNAPTFI	..... G..... TCC..... 1741	
DNAPTR	..... G..... 1750	

FIG. 2F

MAJORITY	[SEQ ID NO:7]	AGAACATCCCCCTCCACCCCTCTGGCTGGGGAGGAGGATCCCCGGCTTCTGGCTGGGGAGGAGGCTGGGT
DNAPTAQ	[SEQ ID NO:1]	.....G.....T.....G.....A.....G.....C.....G.....C.....1814
DNAPTFI	[SEQ ID NO:2]	.....G.....T.....G.....C.....G.....A.....G.....1811
DNAPTR	[SEQ ID NO:3]	.....G.....T.....G.....T.....A.....G.....1820
MAJORITY		GTIGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGTCTGGCCACCTCTGGGGACGAGAACCTG
DNAPTAQ	A.....	A.....G.....A.....G.....C.....A.....1884
DNAPTFI	C.....	T.....C.....T.....T.....C.....1881
DNAPTR	.....	.....A.....G.....A.....A.....1890
MAJORITY		ATCGGGCTTCGAGGGGGAGGACATCCACACCCAGACGGCCAGCTGGATGTTGGGGCTCCCCCGG
DNAPTAQ	.....	.....C.....GG.....
DNAPTFI	.....	.....T.....TT.....C.....1951
DNAPTR	.....A.....	.....A.....A.....A.....A.....1960
MAJORITY		AGGCCGTCACCCCTGATGGCCCCGGCAAGACCATCAACTGGGTCTACGGCATGTCGG
DNAPTAQ	.....	.....G.....
DNAPTFI	A.....GG.....A.....	T.....G.....
DNAPTR	.....	.....G.....G.....C.....
MAJORITY		GCACGCCCTCTCCAGGACCTGGCATCCCTACGGAGGGCTGGCTTCACTGGCCCTACTTCAG
DNAPTAQ	.....	.....A.....T.....CCA.....T.....
DNAPTFI	.....	.....GG.....T.....
DNAPTR	.....T.....A.....G.....	.....T.....A.....A.....2100

**FIG. 2G**

MAJORITY [SEQ ID NO:7]	AGCTTCCCCAAGGTGGGGCTGATTGAGAACCCCTGGAGGAGGGAGGGGGTACGTGGAA							
DNAPTAQ [SEQ ID NO:1]	.....	2164						
DNAPFL [SEQ ID NO:2]	..... A .....	GG .....	..... C .....	..... C .....	..... T .....	.....	2161	
DNAPTR [SEQ ID NO:3]	.....	..... A .....	..... G .....	..... A .....	..... G .....	..... A .....	..... A .....	2170
MAJORITY	CCCTCTTGGGGGGGGCTACGTGGGGACCTAACCCCCGGTGAAGAGCGTGGGGAGGGGGGA							
DNAPTAQ	.....	..... G .....	..... A .....	..... AG .....	..... G .....	..... C .....	..... C .....	2234
DNAPFL	.....	..... T .....	.....	.....	.....	..... C .....	.....	2231
DNAPTR	.....	..... AA .....	..... AA .....	.....	.....	..... CA .....	..... C .....	2240
MAJORITY	GGCGATGGCTTCAACATGGCGTCCAGGCACGGGGACCTCATGAAGCTGGCGATGGTGAACCT							
DNAPTAQ	.....	.....	.....	.....	..... T .....	.....	.....	2304
DNAPFL	.....	.....	..... G .....	.....	.....	..... CG .....	..... T .....	2301
DNAPTR	.....	.....	.....	.....	.....	..... C .....	.....	2310
MAJORITY	TTGGGGGGTXXAGGAATGGGGGGAGGATGCTCTXXAGGTCCACGAGGAGCTGGTGGAGGCC							
DNAPTAQ	..... A .....	..... GG .....	.....	.....	..... T .....	.....	.....	2374
DNAPFL	.....	..... T .....	..... C .....	..... G .....	..... TT .....	..... G .....	..... G .....	2371
DNAPTR	.....	..... G .....	..... G .....	..... G .....	..... G .....	..... C .....	..... C .....	2380
MAJORITY	CCAAAGAGGGGGGGAGGXGGTGGCCGCTTGGCAAGGAGGTATGGAGGGCTATCCCTGGCGT							
DNAPTAQ	..... A .....	..... A .....	..... CC .....	..... CGGC .....	.....	..... G .....	.....	2444
DNAPFL	..... G .....	..... G .....	..... AG .....	..... A .....	.....	..... GG .....	..... CAG .....	2441
DNAPTR	..... C .....	..... C .....	..... C .....	..... A .....	..... G .....	..... AA .....	..... C .....	2450

FIG. 2H

MAJORITY [SEQ ID NO:7] GCGCTGGAGCTGGAGTGGGGAGGACTGGCTCTGGGCAAGGAGTAG

DNAPTAQ [SEQ ID NO:1] ..... A ..... G  
DNAPTF1 [SEQ ID NO:2] ..... G ..... A  
DNAPTF2 [SEQ ID NO:3] ..... T ..... G

**FIG. 3A**

MAJORITY	[SEQ ID NO:8]	MXAMPLFEPKGRLVLDGHHLAYRTFFALKGLTSRGEPVQAVYFAKSLLKALKEG-DANVXWVFDAK
TAQ PRO	[SEQ ID NO:4]	RG.....H.....H.....I.....V.....V..... 69
TFL PRO	[SEQ ID NO:5]	.....V.....V..... 68
TTA PRO	[SEQ ID NO:6]	E.....YK.....F..... 70
MAJORITY		APSFRHEAYEAYKAGRPTPEDFPROLALIKELVDLGLYXLEVPGYEADDVLATIAKKAEEKEGYEVRI
TAQ PRO		.....GG.....A.....V.....S..... 139
TFL PRO		.....V.....F.....R..... 138
TTA PRO		.....FT.....L.....K..... 140
MAJORITY		TABRDLYOLLSPRIAVLHPFGYLITPAWLWEKYGLRPEOWDYLRAKGPPSDNLPGVKGIGEKTAXKLX
TAQ PRO		.....K.....H.....D.....A.....T.....E.....R.....E..... 209
TFL PRO		.....E.....I.....Y.....A.....I.....A.....R..... 208
TTA PRO		.....V.....V.....H.....E.....F.....V.....L.....K..... 210
MAJORITY		EWGSLENLKNLDRVKP-XXREKIXAHMEDLXLXXLSXVRDOLPLEDFAXRREPREGRLRAFLERLEF
TAQ PRO		.....A.....L.....AI.....L.....D.....K.....WD.....AK.....K.....R..... 278
TFL PRO		.....FOH.....O.....SL.....LG.....A.....A.....RK.....Q.....H.....GR.....T.....NL..... 277
TTA PRO		.....ENV.....K.....L.....R.....LE.....R.....L.....L.....OG..... 280
MAJORITY		GSLLHEFGLEXPKALEEAPWPPPEGAFVGFLVLSRPEPMWAELLALAAARRXGRVHRAKDPLXGLRDLKEV
TAQ PRO		.....S.....K.....D.....G.....PE.....YKA.....A..... 348
TFL PRO		.....G.....A.....L.....SF.....G.....WE.....L.....Q.....R.....G..... 347
TTA PRO		.....A.....AP.....G.....K.....G.....D.....A.....A.....K..... 350

FIG. 3B

MAJORITY	[SEQ ID NO:8]	RGLLAKDLAVLAREGLDLXPDDPMMLAYLLOPSNTPEGVARRYGGEWTEDAGEALLSERLFXNLXX
TAQ PRO	[SEQ ID NO:4]	S. G. P. E. A. A. WG 418
TFL PRO	[SEQ ID NO:5]	I. F. E. A. OT. KE 417
TTR PRO	[SEQ ID NO:6]	S. V. AH. HR. LK 420
MAJORITY	RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDNAYLQALSLEVAAEIRRLEEVFRLAGHPFNLNSRD	
TAQ PRO		R. R. A. R. A. A. A. 488
TFL PRO		K. E. R. EA. V. Q. 487
TTR PRO		K. H. L. 490
MAJORITY	QLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILORYRELLKLKNTYIDPLIXLVRHPTG	
TAQ PRO		S. D. I. 558
TFL PRO		DR. A. K. 557
TTR PRO		R. I. Q. H. V. S. 560
MAJORITY	RLHTRFNOTATATGRLSSSDPNLONIPURTPLGORIRRRAFAEEGWWXLVALDYSQIELRVLAHLSDENL	
TAQ PRO		I. L. V. V. 628
TFL PRO		V. V. 627
TTR PRO		A. A. 630
MAJORITY	IRVFGEGRDIHTOTASHMFGNPPEAVNDPLMRRAAKTINFGVLYGMSAHLSSOELAIPIYEEAVAFIERYFO	
TAQ PRO		E. R. 0. 698
TFL PRO		S. G. G. S. 697
TTR PRO		K. V. 700

FIG. 3C

MAJORITY [SEQ ID NO:8] SFPKVRAWI EKTL EGR RRGYVET LFGRRRYV PDLNARVKS VREAERMA FNMPVQGTAADL MKLAMWKL

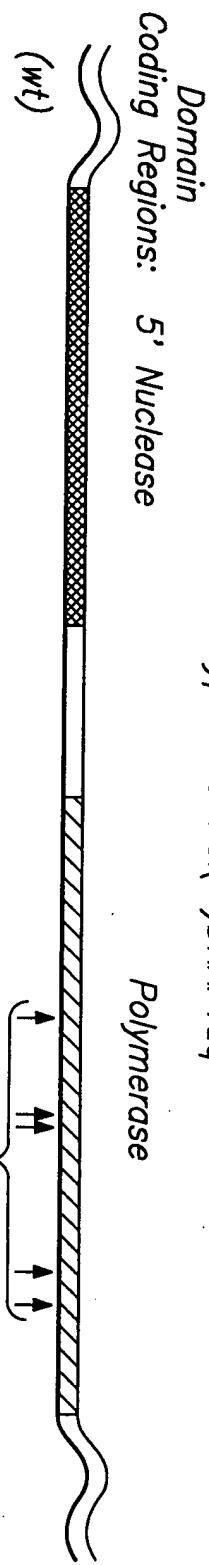
TAQ PRO	[SEQ ID NO:4]	E	768
TFL PRO	[SEQ ID NO:5]	Y	
TTR PRO	[SEQ ID NO:6]	G	767
		K	770

MAJORITY FPRLXEMGARMILQVHDELVLEAPKXRAEXVAALAKEVME GYVPLAVPLEEVNGXGEDWLSAKEY

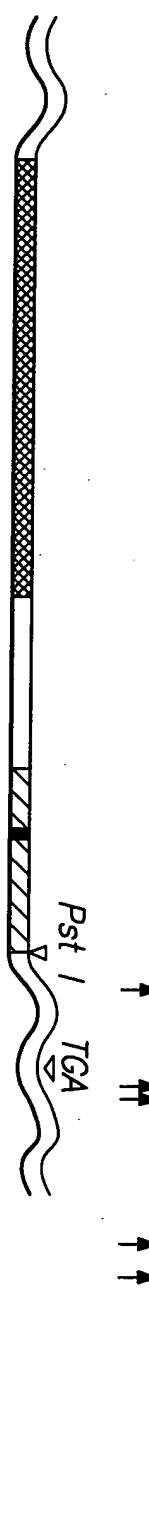
TAQ PRO	E	E	833
TFL PRO	Q	A	
TTR PRO	L	R	831
	D	W	
	R	Q	
	R	L	
	L	A	
	Q	E	
	A	K	
	M	K	
	G	G	835

Genes for Wild-Type and *PoI(-)DNAPTag*

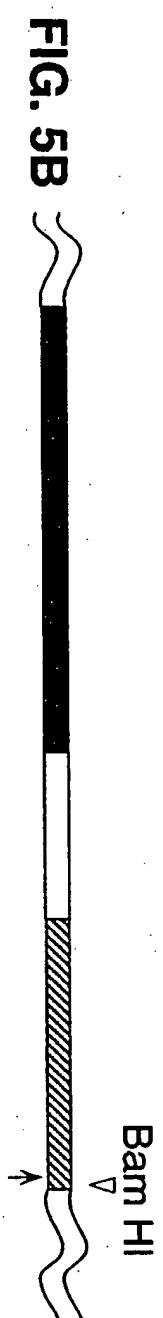
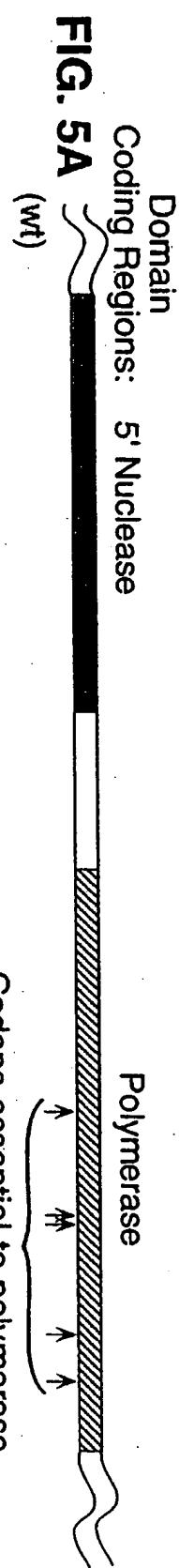
**FIG. 4A** Coding Regions: 5' Nuclease

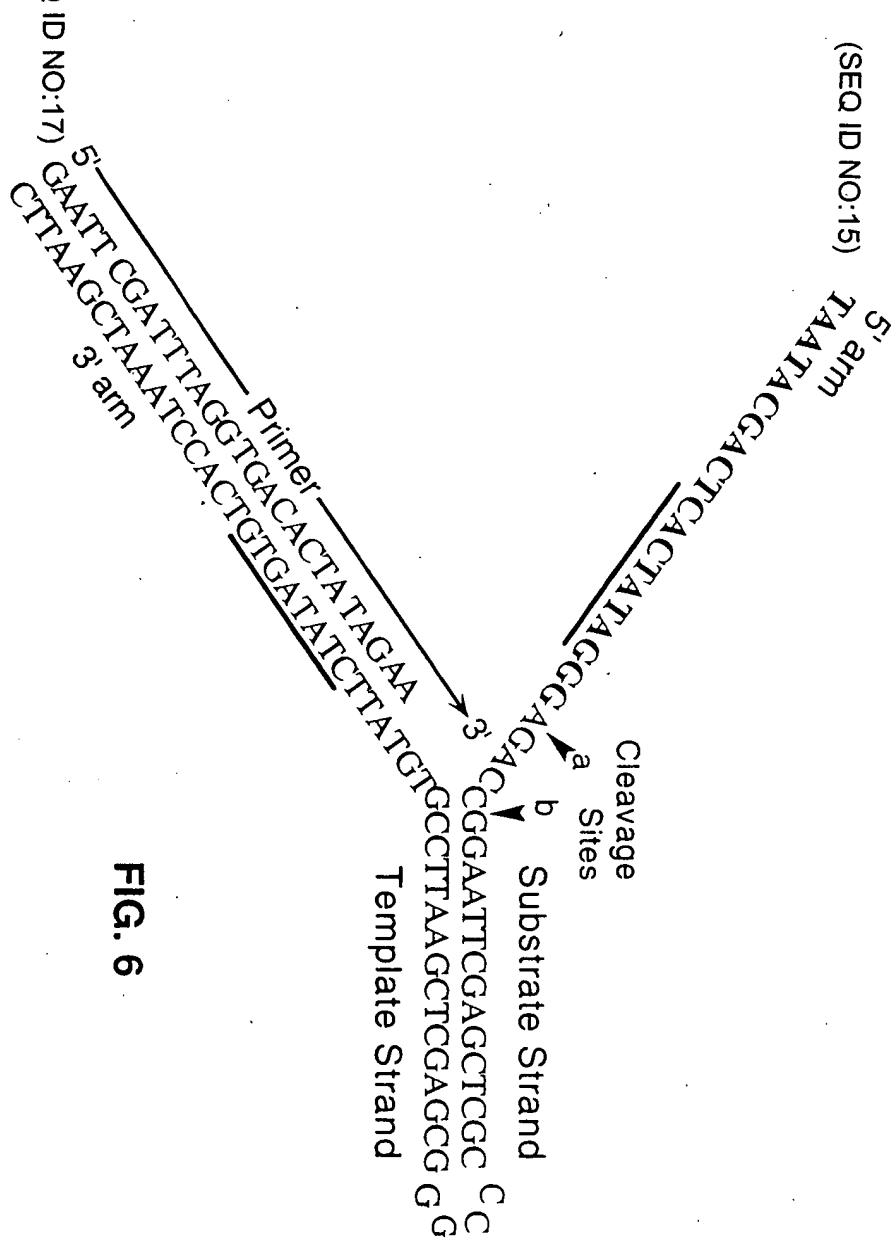


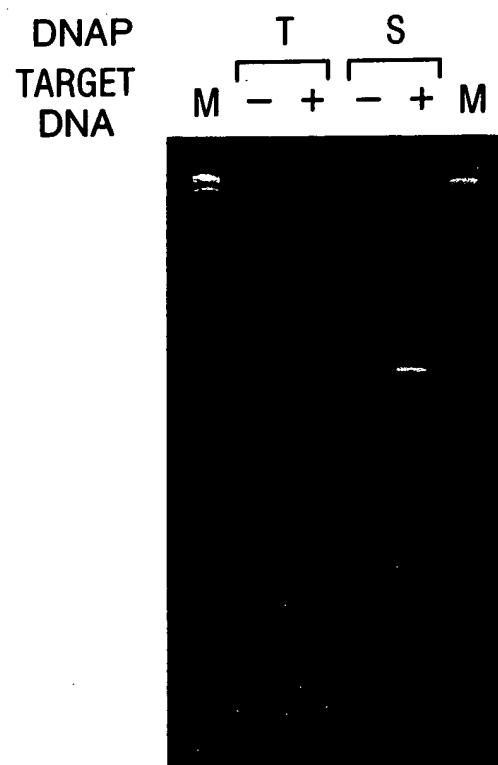
**FIG. 4B**



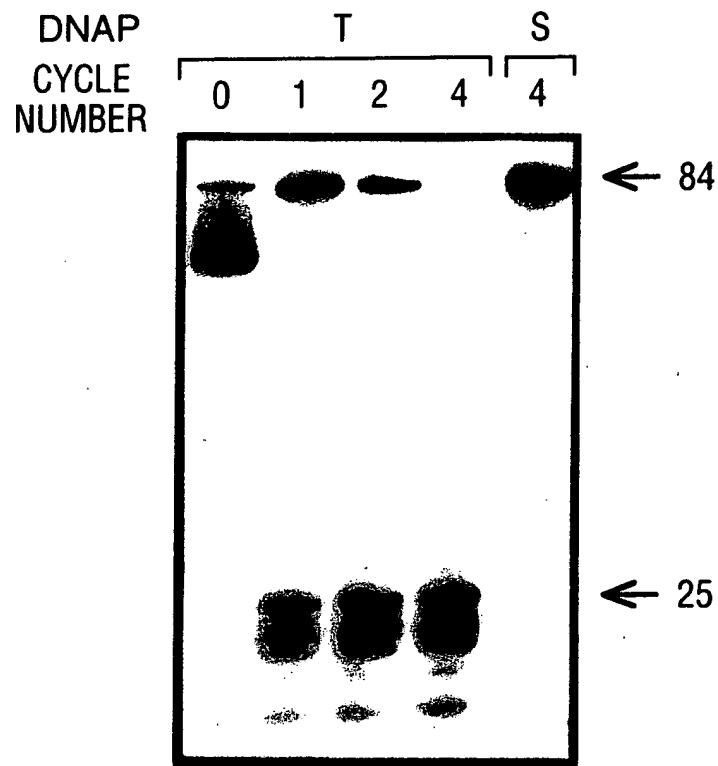
### Genes for Wild-Type and Pol(-) DNAP<sub>T</sub><sup>fl</sup>





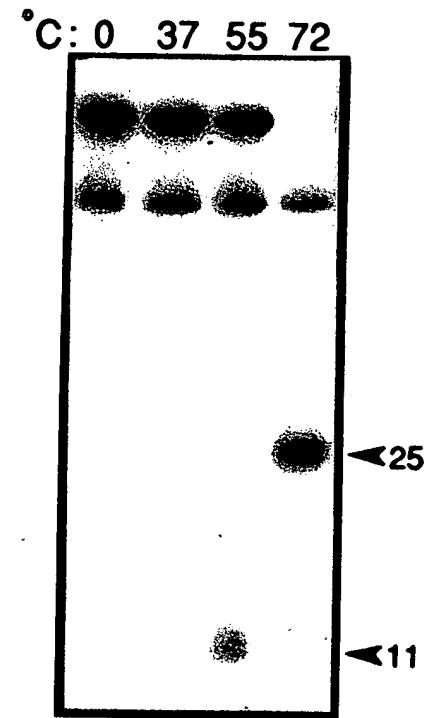
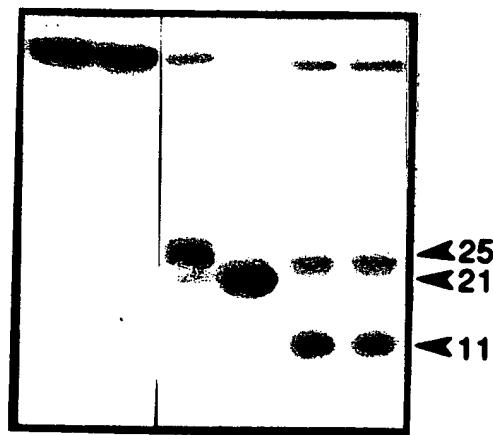


**FIG. 7**



**FIG. 8**

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl <sub>2</sub> :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-



"Replacement Sheet"

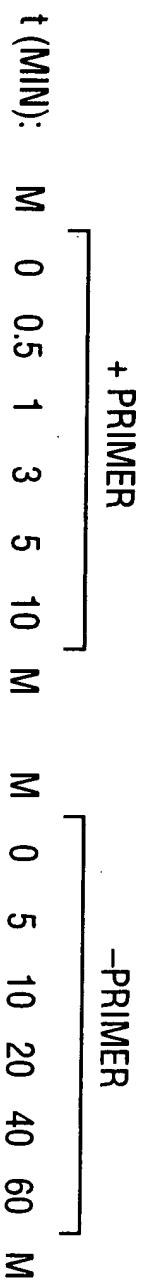
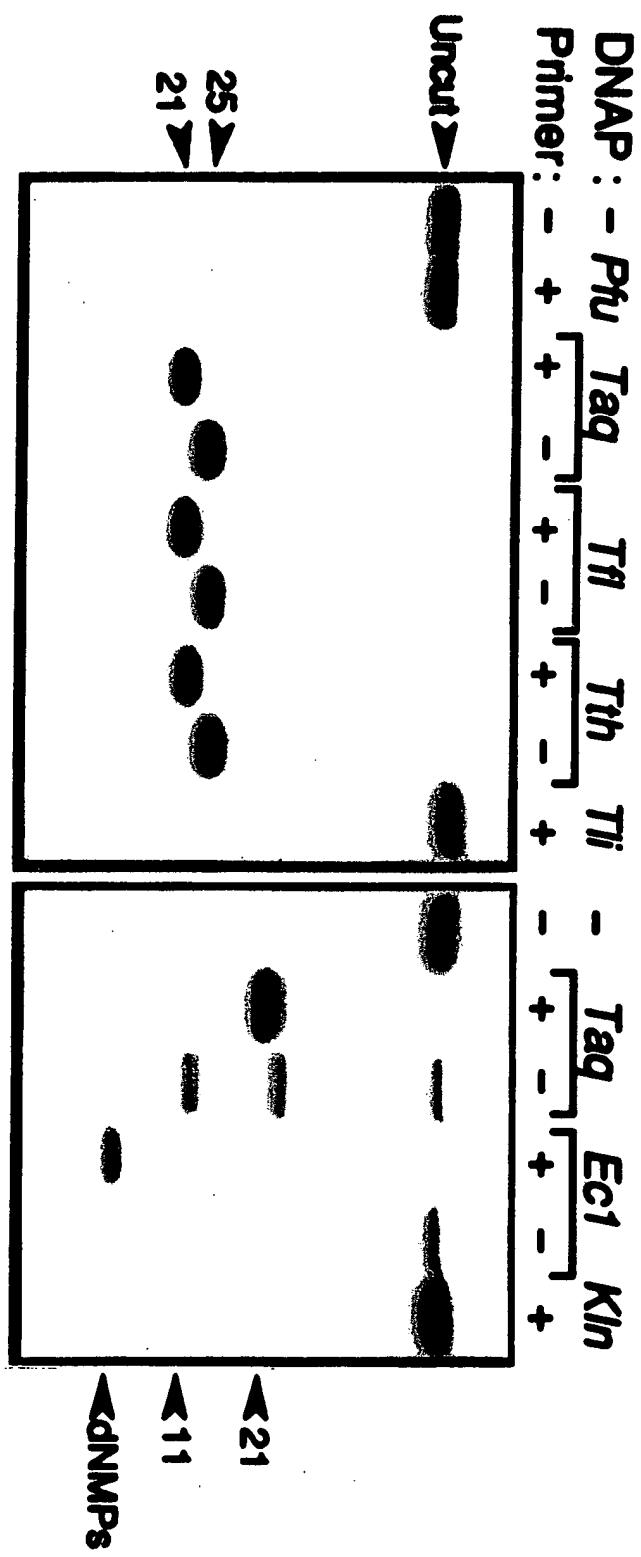
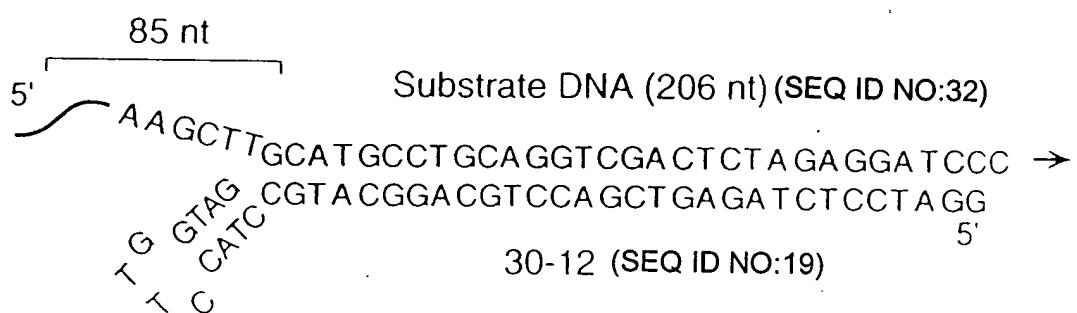
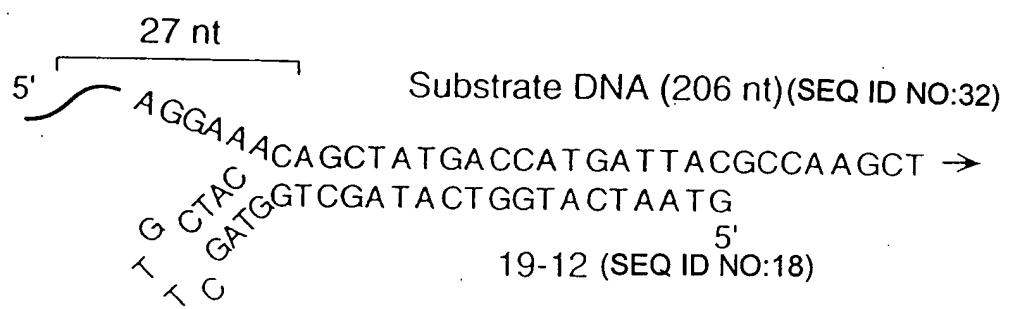


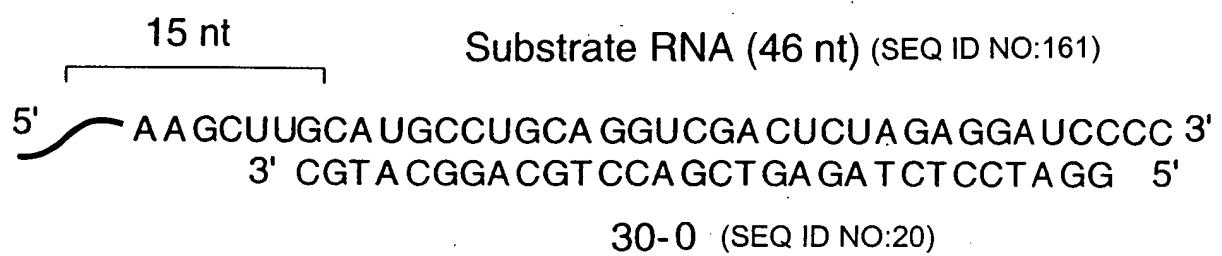
FIG. 10A

FIG. 10B



## FIG. 12A





**FIG. 13A**

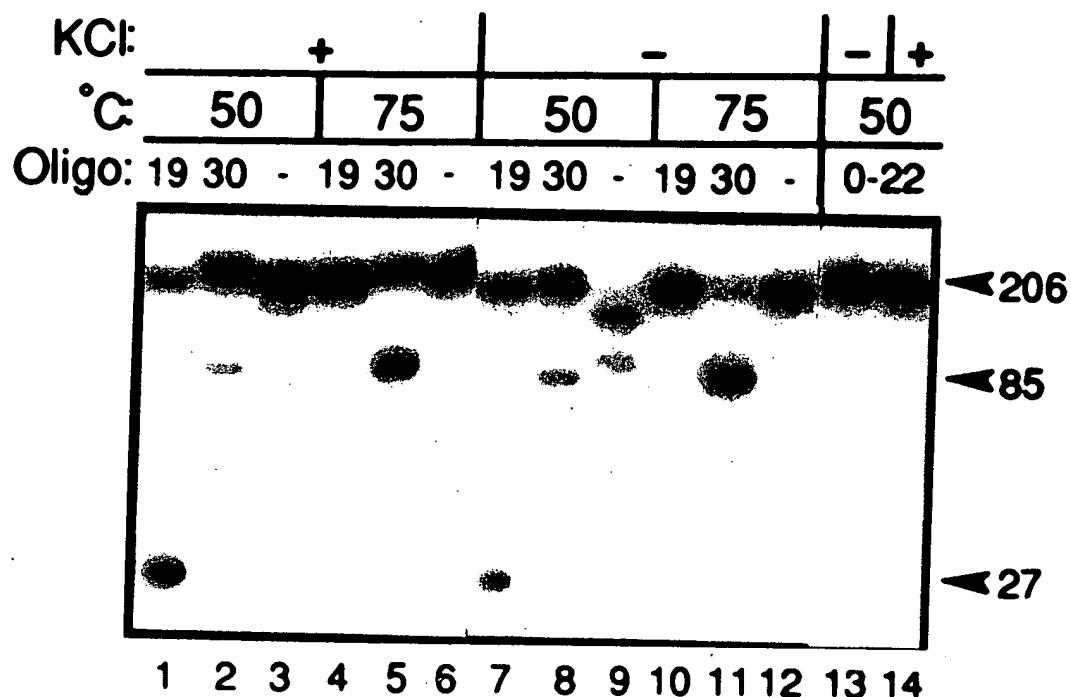


FIG. 12B

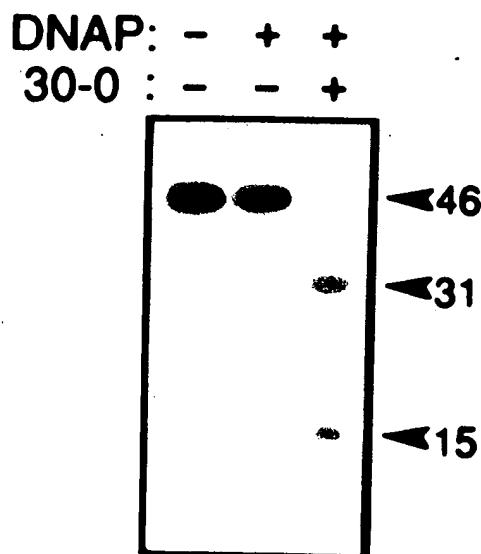


FIG. 13B

(SEQ ID NO:162)

TTGACAATTAATCATCGGCTCGTATAATGTGTGGAATGTGAGGGATAACAATTCACACAGGAACAGCG  
 -35  
 -10  
 RBS  
 MetAsnSer...  
 ATGAATTCGAGCTCGTACCCGGGATCCTCTAGAGTCGACCTGCAGGCATGCAAGCTGGCACTGCC  
 EcorI \_\_\_\_\_ KpnI \_\_\_\_\_ BamHI \_\_\_\_\_ Sall \_\_\_\_\_ SphI \_\_\_\_\_ PstI \_\_\_\_\_ HindIII  
 SstI      SmaI      XbaI

FIG. 14B

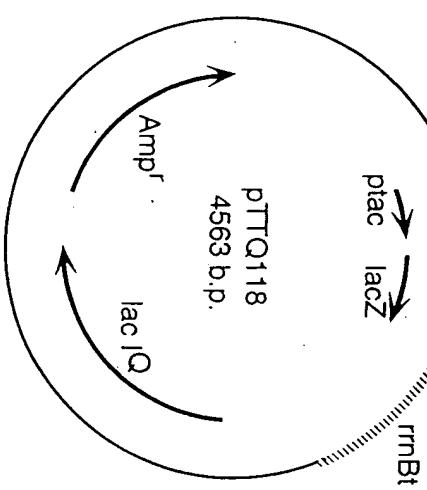


FIG. 14A

RBS: Ribosome binding site  
ptac: Synthetic tac promoter  
lacIQ: Lac repressor gene

lacZ: Beta-galactosidase alpha fragment  
rrnBt: *E. coli* rrnB transcription terminator

FIG. 14C

(SEQ ID NO:163)

AGATCTCGATCCCGCGAAATTAAATACGACTCACTATAGGGAGACCACAAACGGTTCCCTCTAGAAATAATTGTTT  
Bgl II T7 Promoter XbaI

AACTTAAAGAAGGAGATATACATATGGCTAGCATGACTGGTGGACAGCAAATGGTCGGATCCGGCT  
RBS MetAlaSer NdeI

NdeI

T $\phi$

BamHI

FIG. 15B

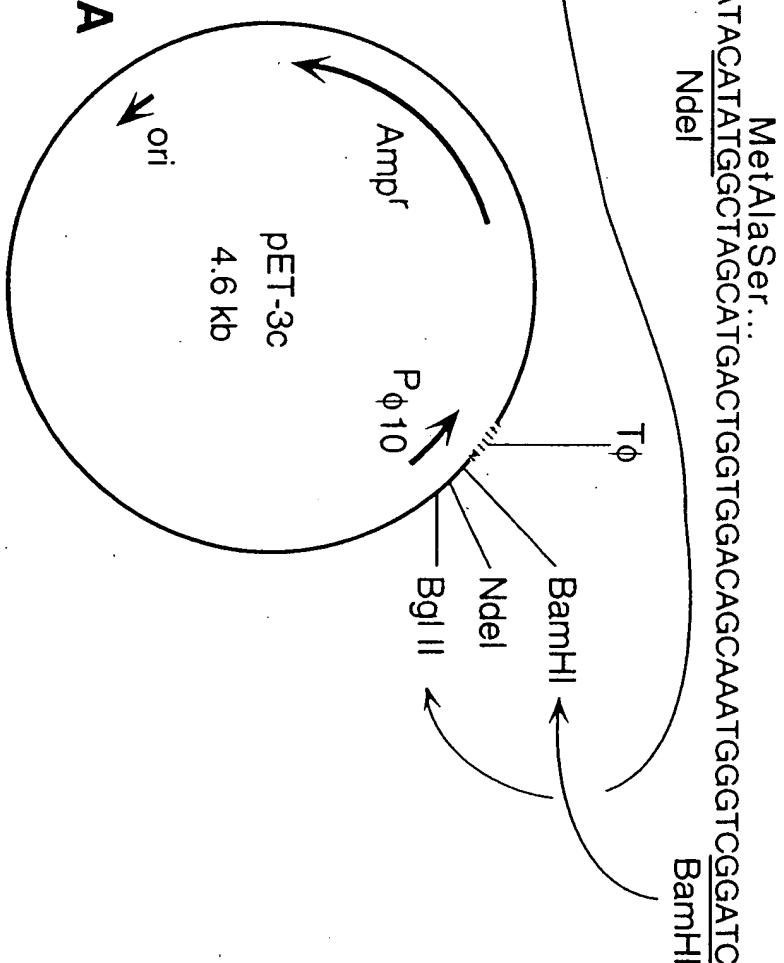
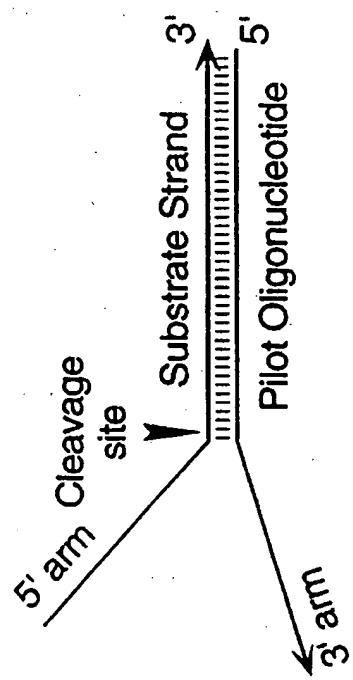


FIG. 15A

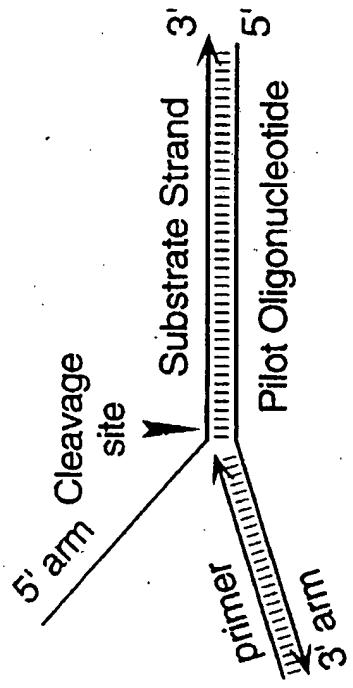
RBS: Ribosome binding site

$P_{\phi 10}$ : Bacteriophage T7  $\phi 10$  promoter  
 $T_{\phi}$ : T7  $\phi$  Terminator

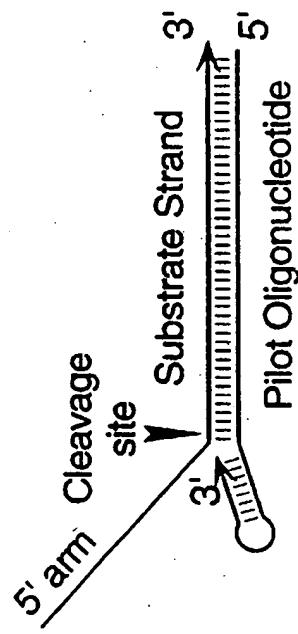
FIG. 15C



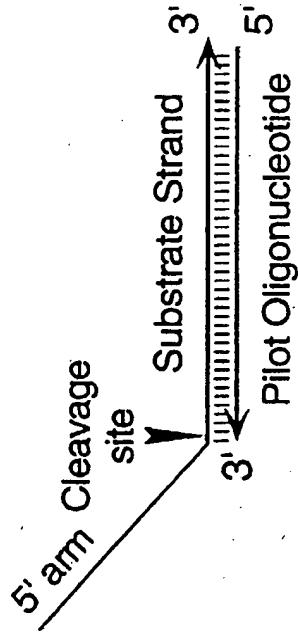
**FIG. 16A**



**FIG. 16B**



**FIG. 16C**



**FIG. 16D**

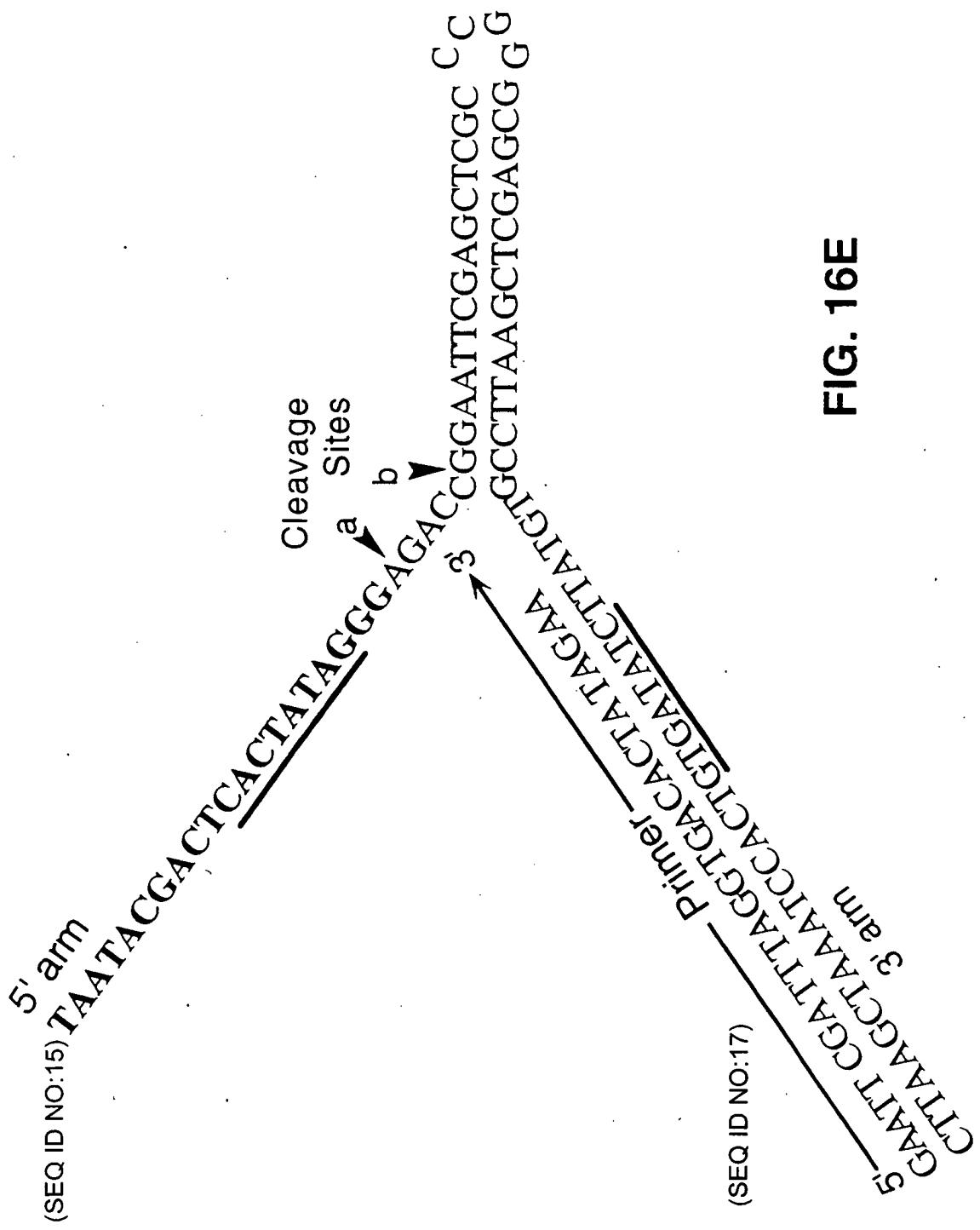


FIG. 16E

1 2 3 4 5 6 7

} UNCLEAVED SUBSTRATE

} CLEAVED SUBSTRATE

- - - + - - + dNTPs  
- - + + - - + PRIMER  
Taq 4e 5b ENZYME

"Replacement Sheet"

**FIG. 17**

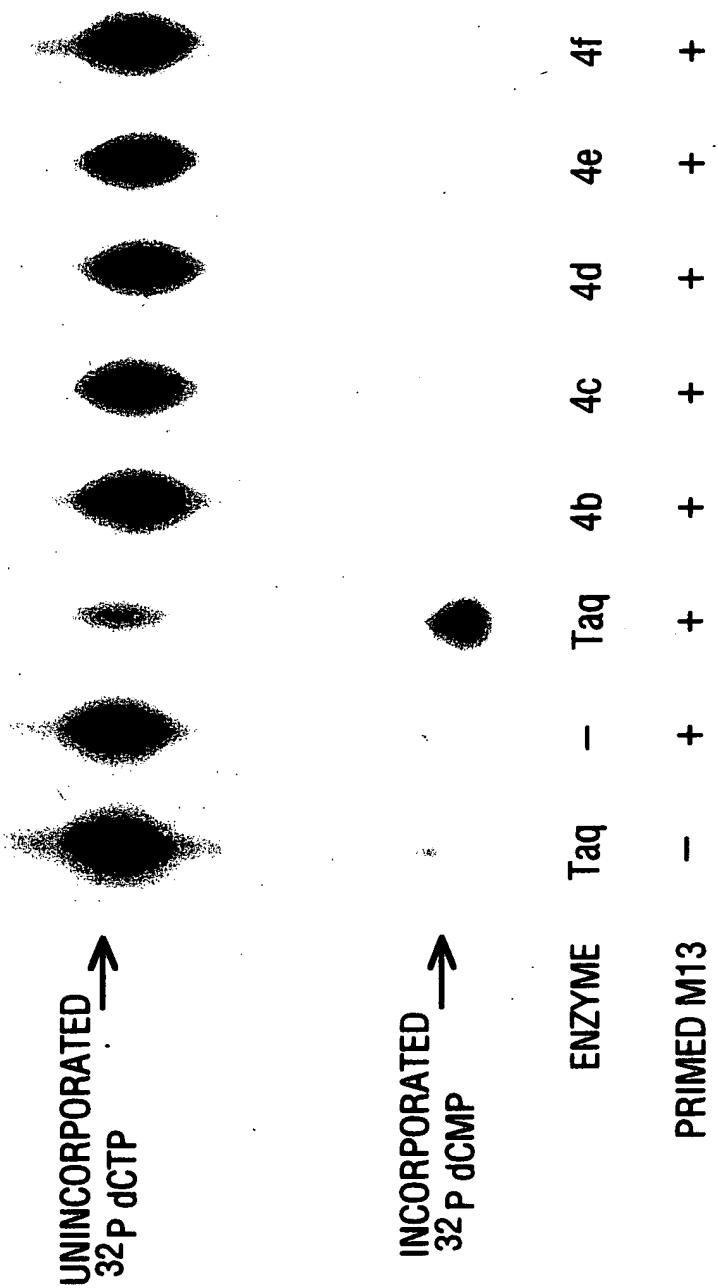
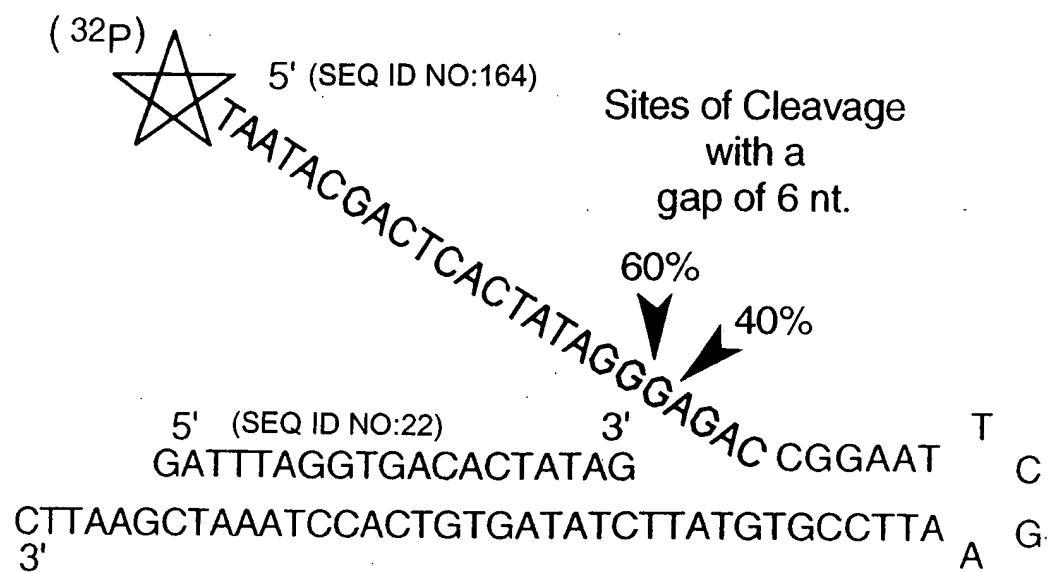


FIG. 18



**FIG. 19A**

		"4d"		"4b"		UNMODIFIED	
		NO POL. ACTIVITY		MUTATION SMALL ACTIVITY		DNAP Taq	
1	2	3	4	5	6	7	8
-	-	-	+	-	+	-	+

dNTP

84 NUC. —



HAIRPIN TEST MODULE

CONVERSION TO DOUBLE STRANDED  
(COMPLETE EXTENSION OF PRIMER)

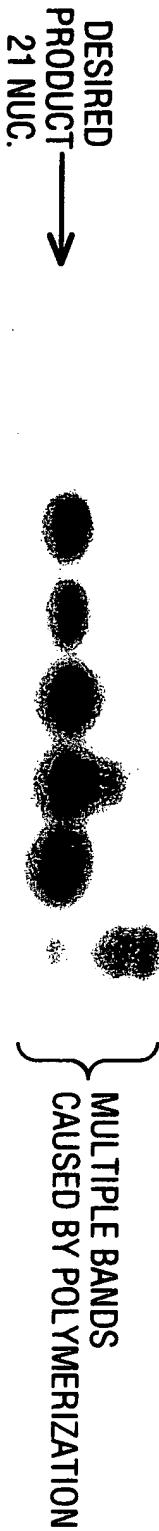


FIG. 19B

↑ SOME ABERRANT CLEAVAGE WITH "4b"  
BECAUSE OF RESIDUAL POLYMERASE ACTIVITY.

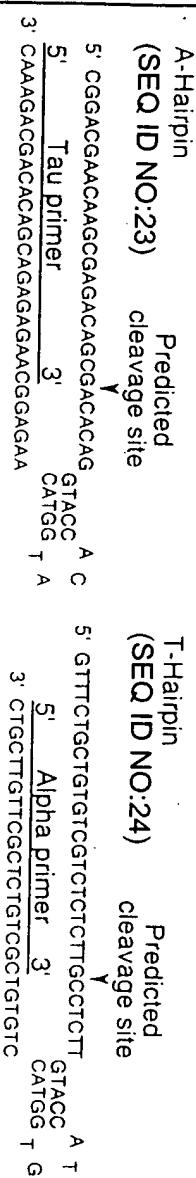


FIG. 20A

Sequence of alpha primer: (SEQ ID NO:25)  
5' GACGAAACAAGCGAGACAGCG 3'

FIG. 20B

3' CAAAGACGACAGCAGAGAGAACGGAGA 5' Tau primer 3' CTA  
**FIG. 20C** Cleaved A-Hairpin 5' CCTCTT GTACC A T  
 3' CTACTTGTGCTGTGCTGTGTC 5' Alpha primer 3' CATGG T G

FIG. 20C

Sequence of alpha primer: (SEQ ID NO:25)  
5' GACGAAACAAGCGAGACAGCG 3'

FIG. 20B

3' CAAAGACGACAGCAGAGAGAACGGAGA 5' Tau primer 3' CTA  
**FIG. 20C** Cleaved A-Hairpin 5' CCTCTT GTACC A T  
 3' CTACTTGTGCTGTGCTGTGTC 5' Alpha primer 3' CATGG T G

FIG. 20C

**FIG. 20C**

**Tau primer**

5' CAAAGACGACAGCAGAGAACGGAGAA 3'

**Alpha primer**

5' CTGCTTGTGCTCTGTCGCTGTC 3'

**Cleaved A-Hairpin**

**Cleaved T-Hairpin**

**(SEQ ID NO:28)**

**(SEQ ID NO:27)**

5' GTTCTGCTGTCTCTTGCCCTTGTA  
3' CAAAGACGACACAGCAGAGAACATGGTACACCATGGACACAGGGACAGAGGGAA  
5' CAGAGCAGAGGGAA  
EIG 200 T-Hairpin

FIG. 20D

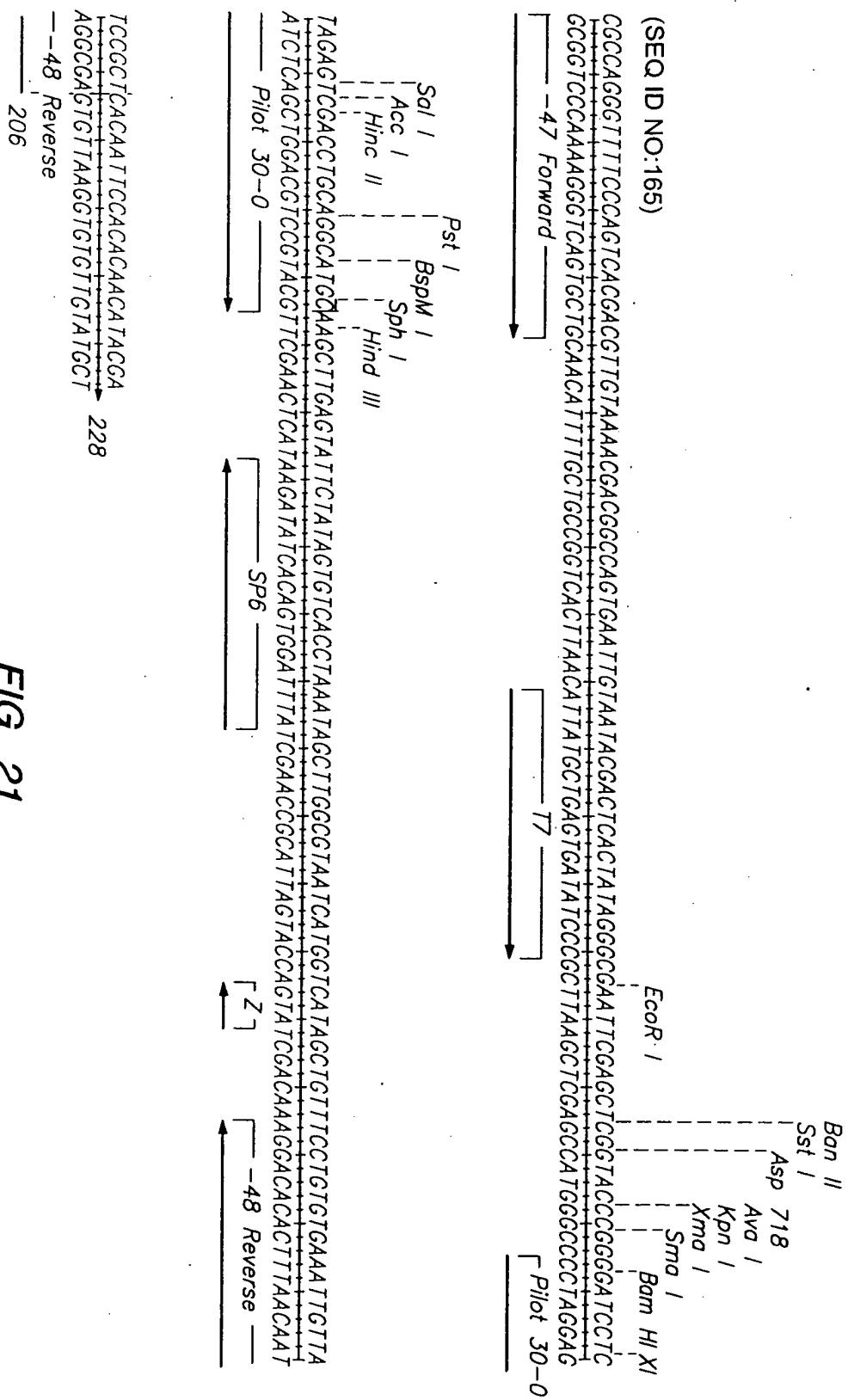
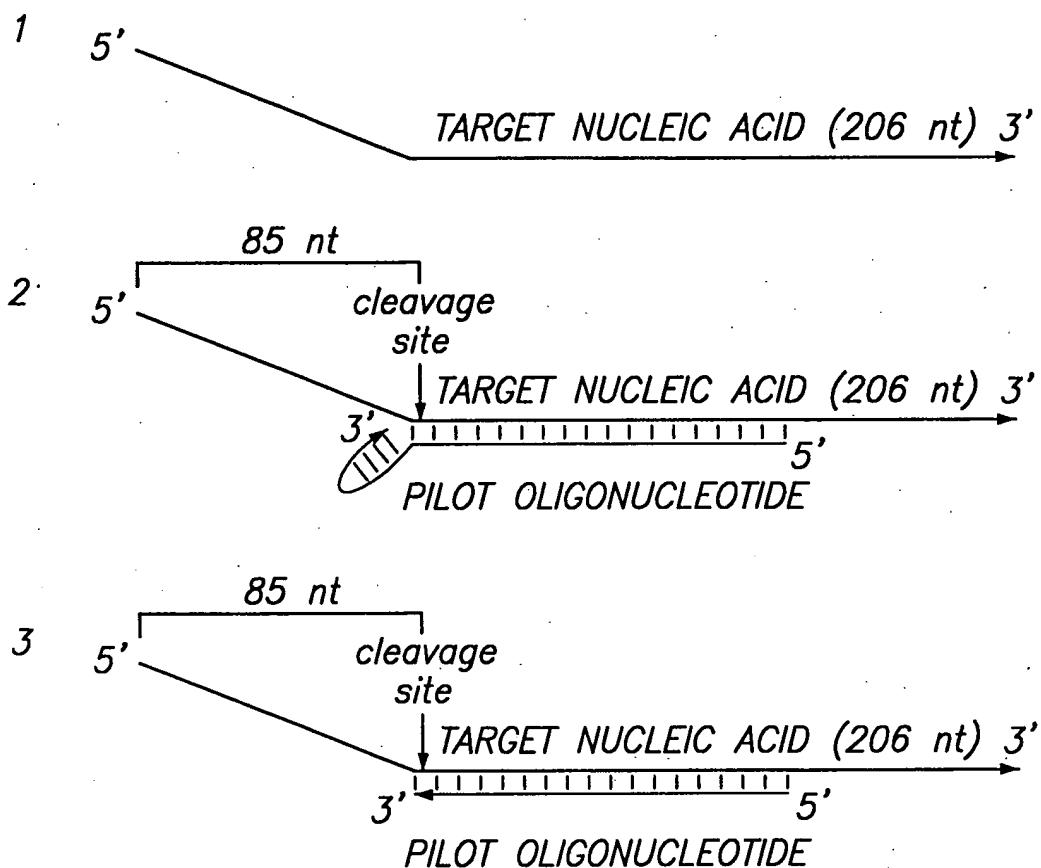


FIG. 21



**FIG. 22A**

## "Replacement Sheet"

I	II	III	IV	V	I	VI
1	1	2	3	1	2	3
1	1	2	3	1	2	3
1	1	2	3	1	2	3
1	1	2	3	1	2	3

**FIG. 22B**

## "Replacement Sheet"

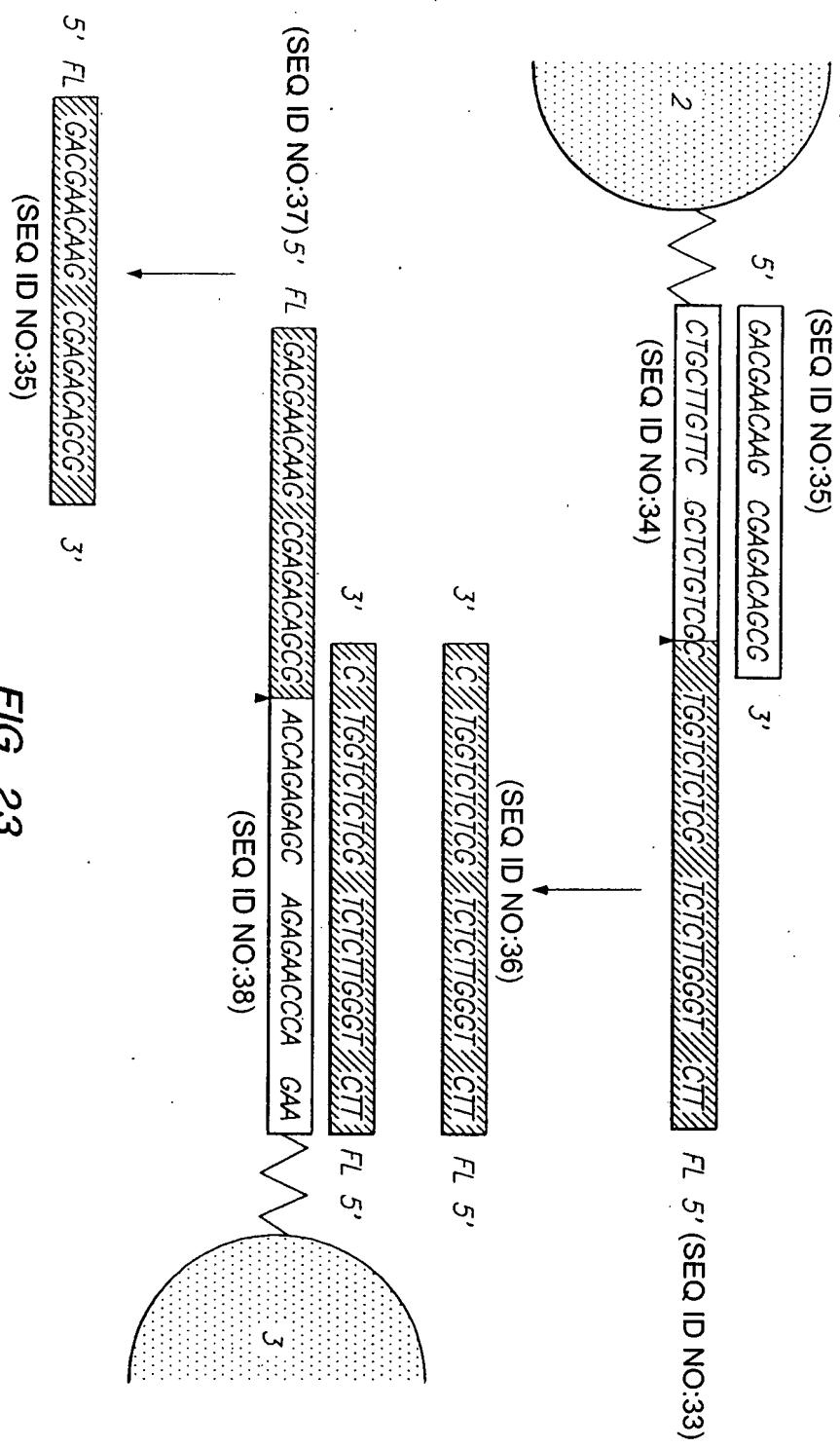
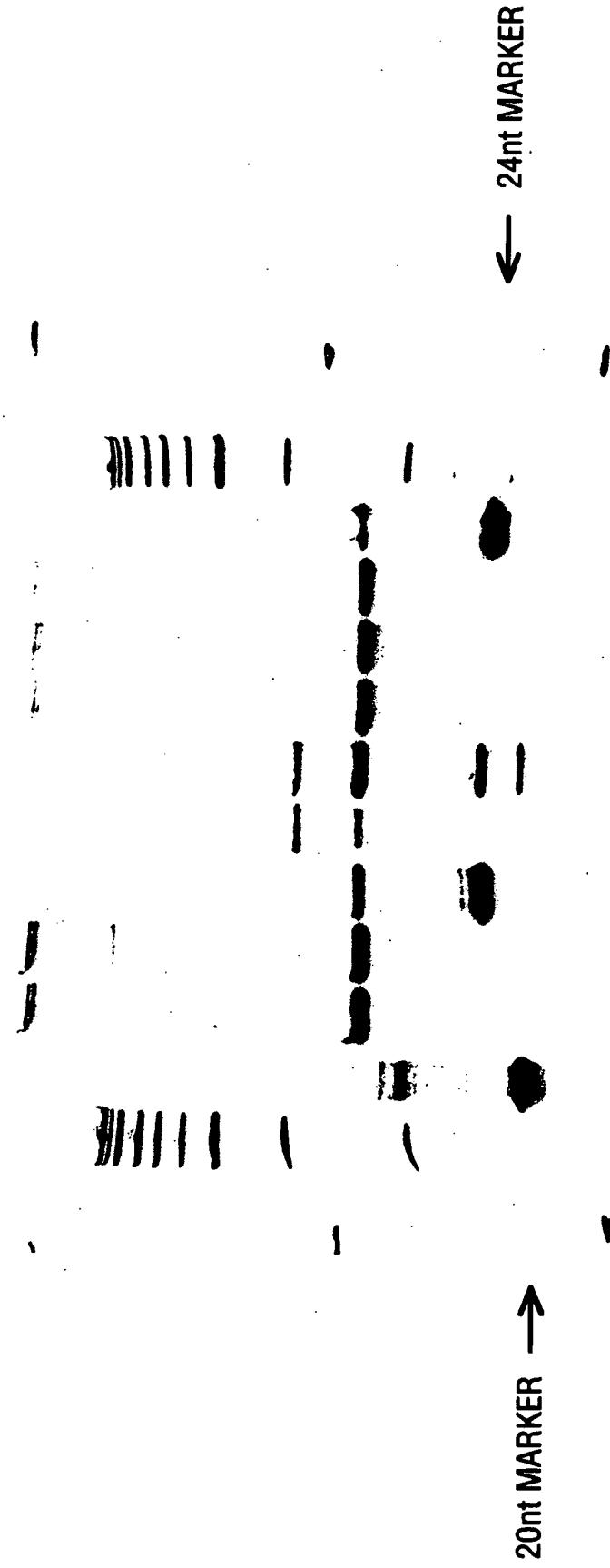


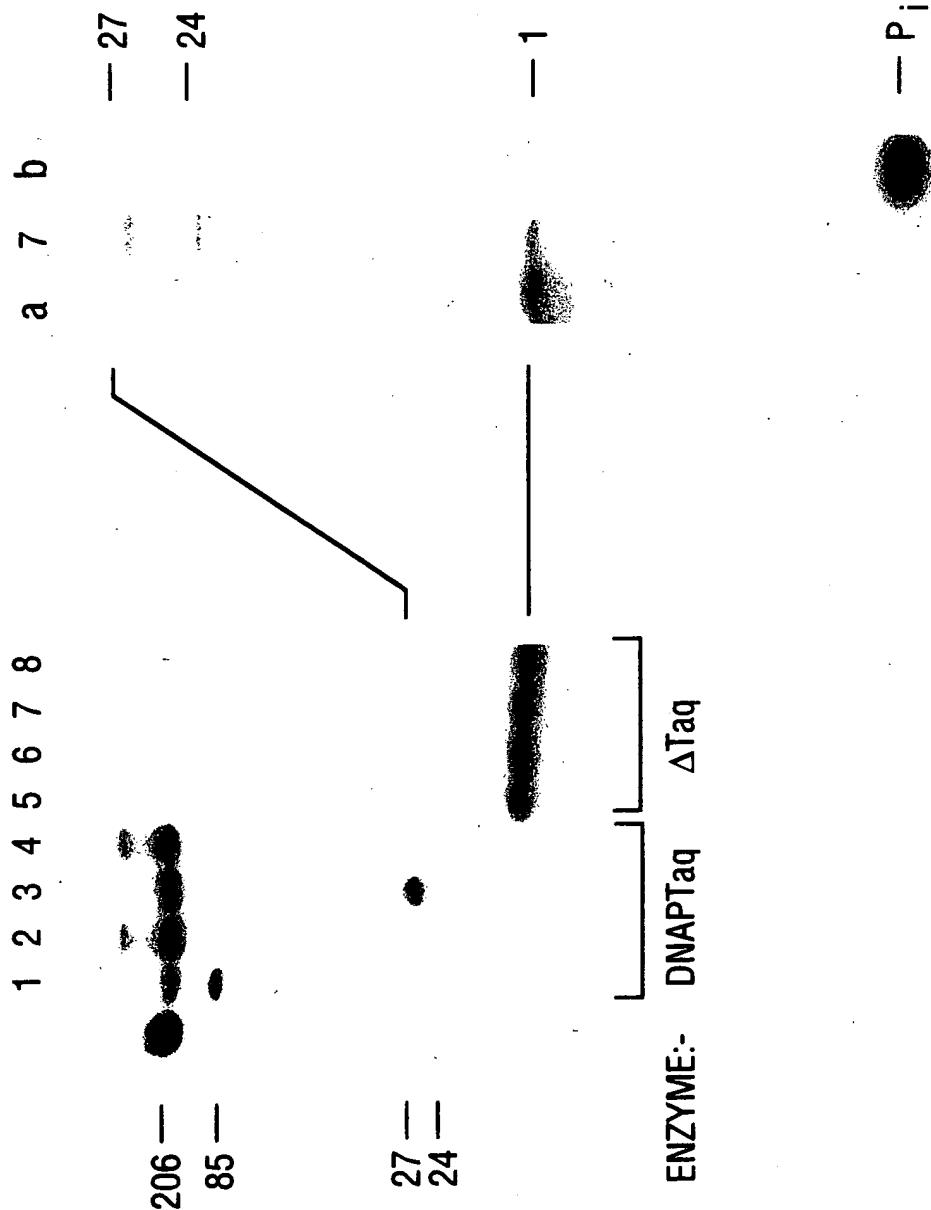
FIG. 23

CDR BEAD	T	T	T	A/T	A/T	A	A	A
PILOT	-	-	+	-	+	-	-	-
CLEAVASE	M	M	-	+	+	+	+	-



"Replacement Sheet"

FIG. 24



**FIG. 25A**

**FIG. 25B**

FIG. 26A

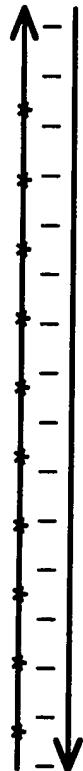
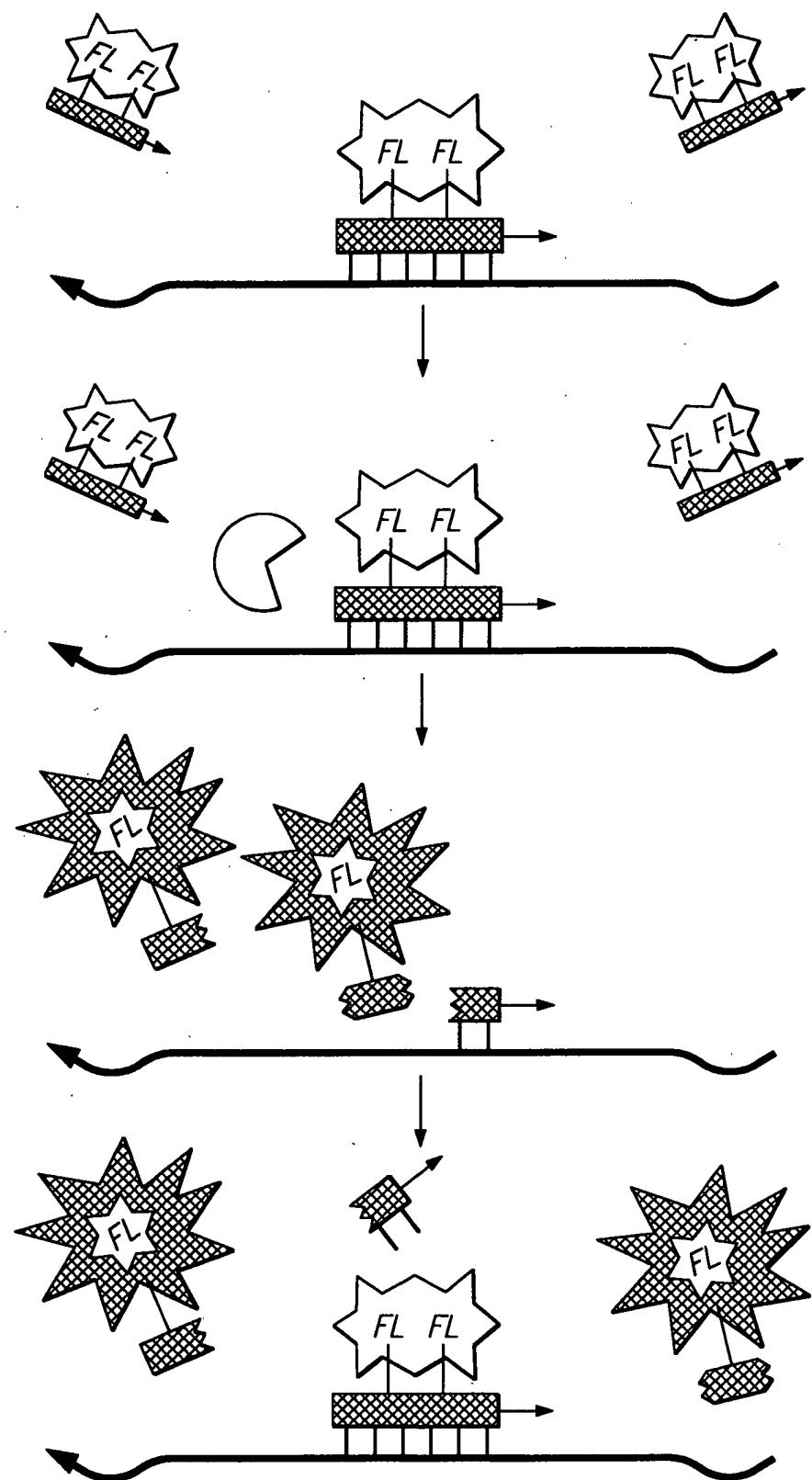


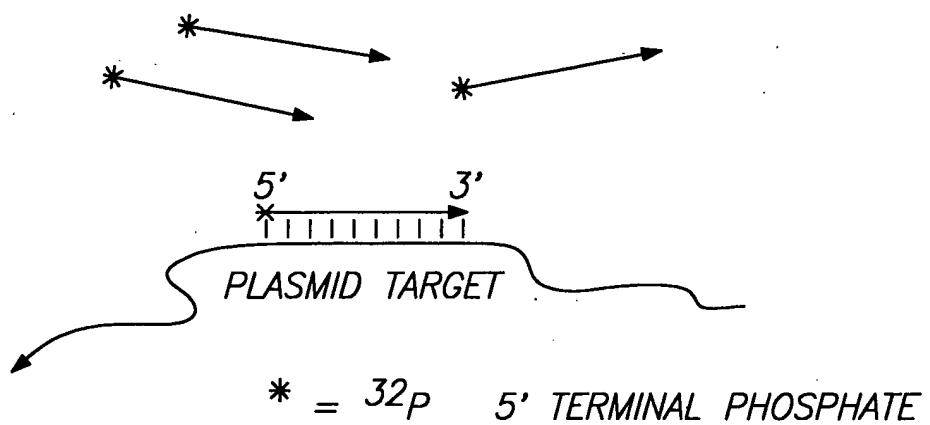
FIG. 26B

\* = 32p





**FIG. 27**



**FIG. 28A**

M 1 2 3 4 5 6

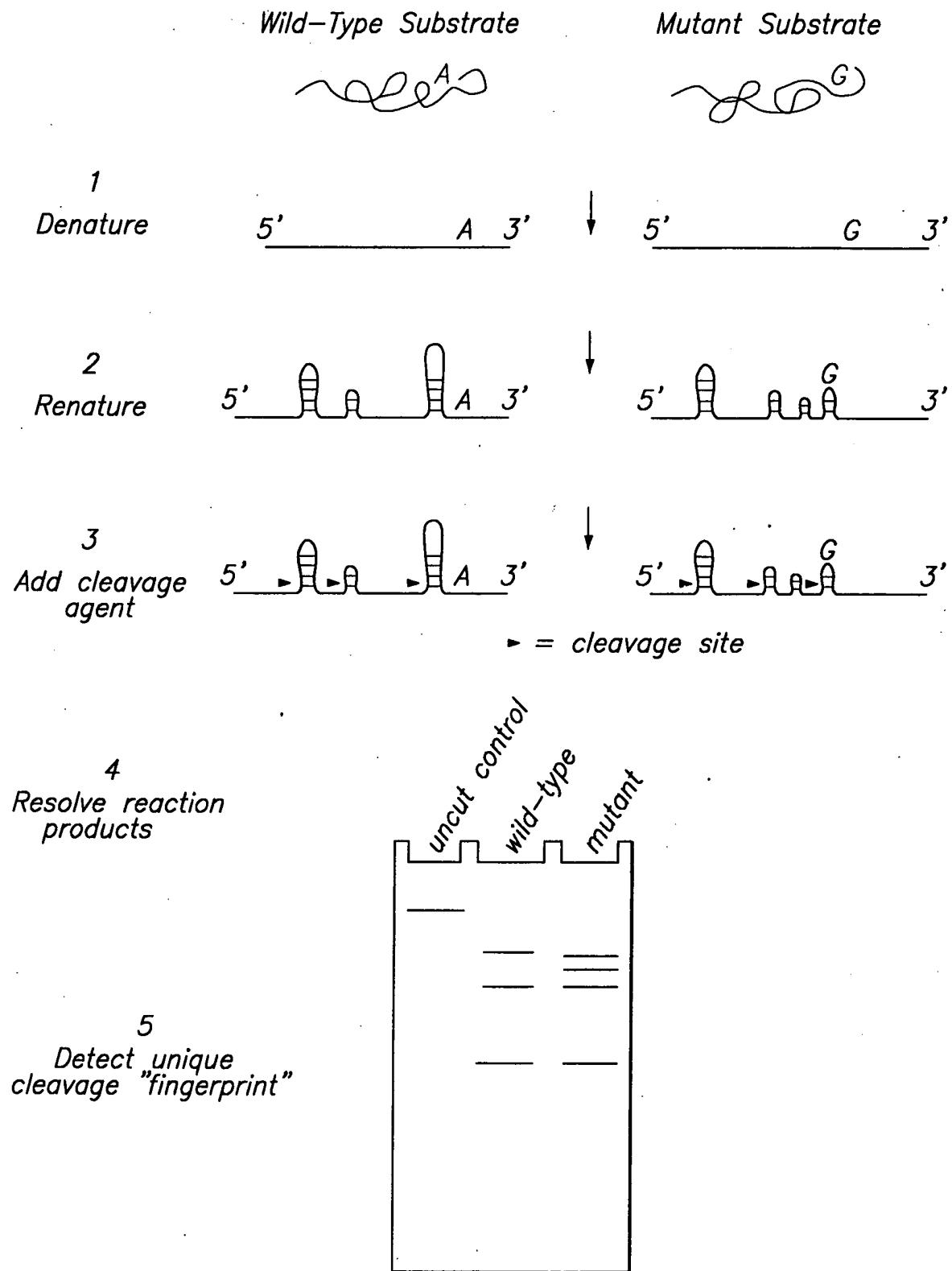


— 21



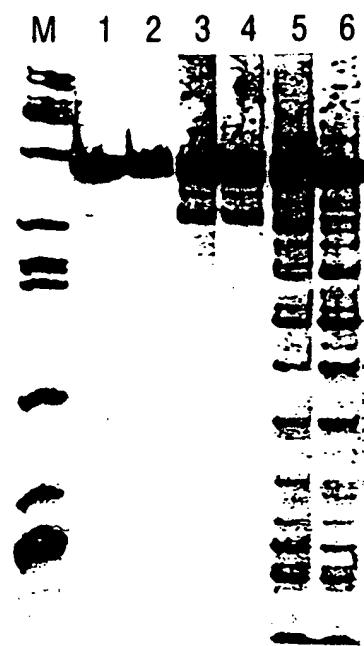
— 1

**FIG. 28B**



**FIG. 29**

## "Replacement Sheet"



**FIG. 30**

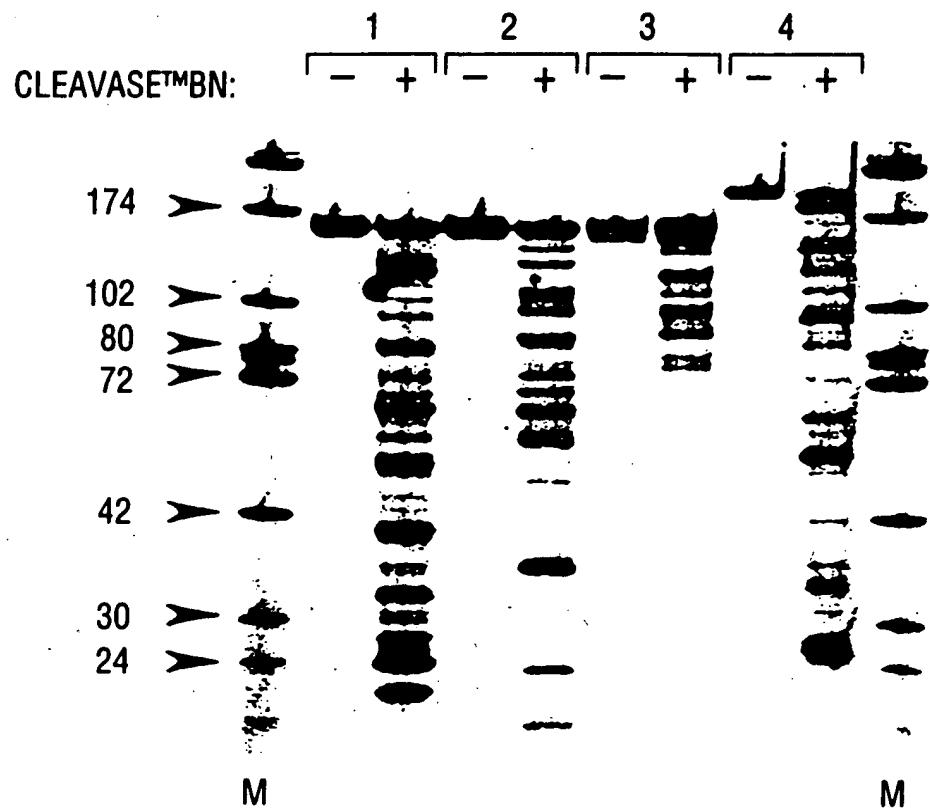


FIG. 31

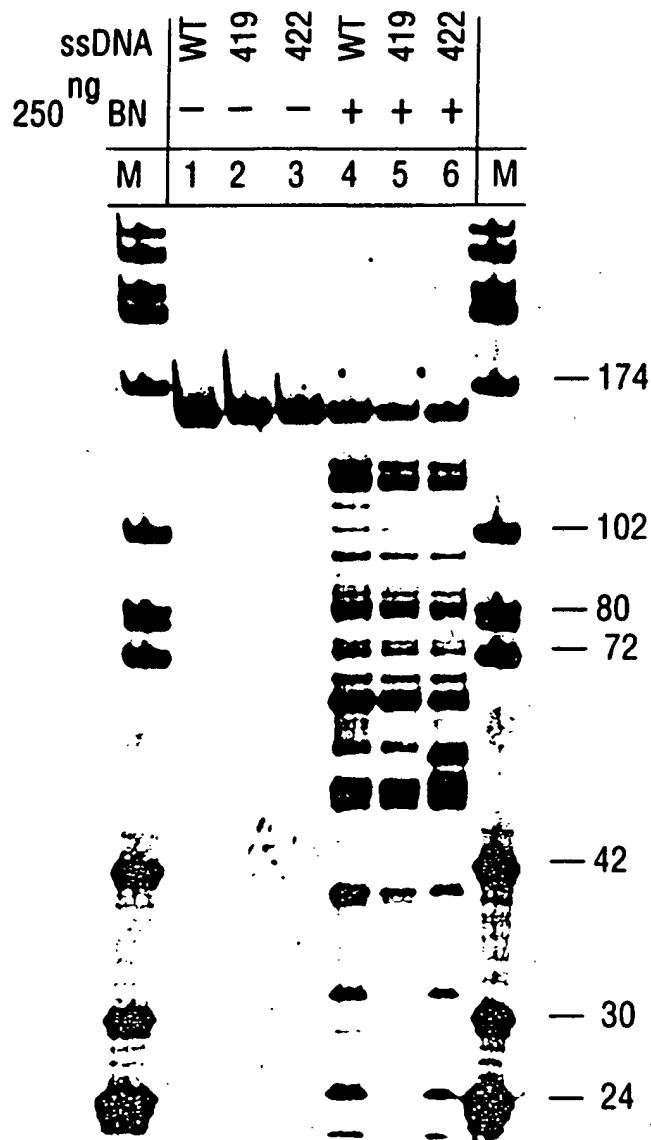


FIG. 32

"Replacement Sheet"

157 378 1056 1587  
M 1 2 3 4 5 6 7 8 M



WT 422  
WT 422  
WT 422  
WT 422

FIG. 33

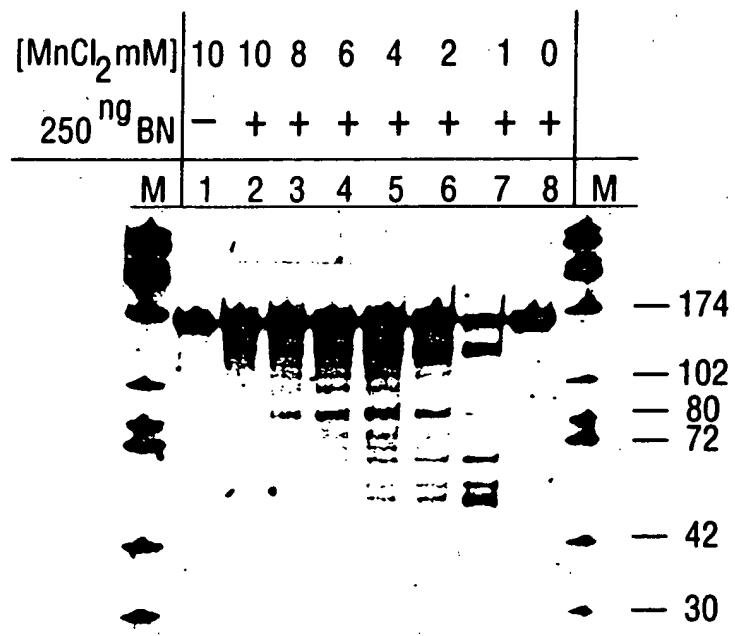
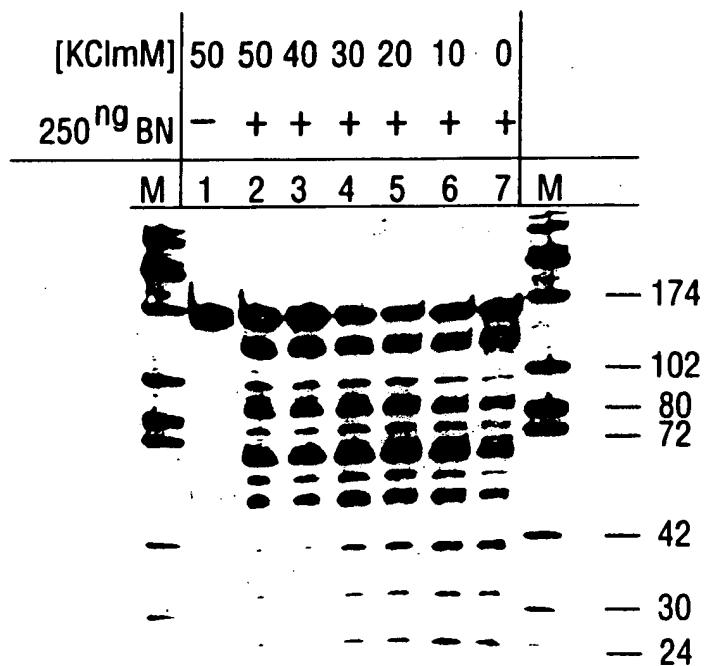


FIG. 34



**FIG. 35**

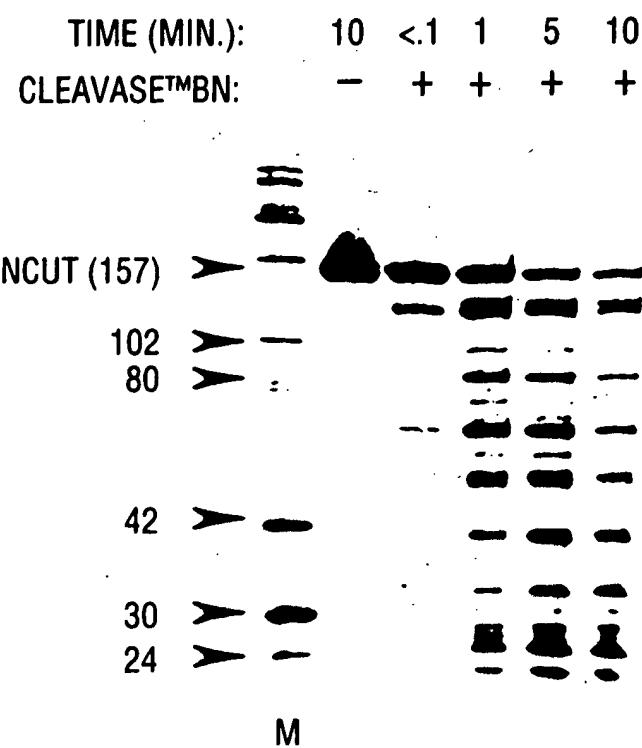
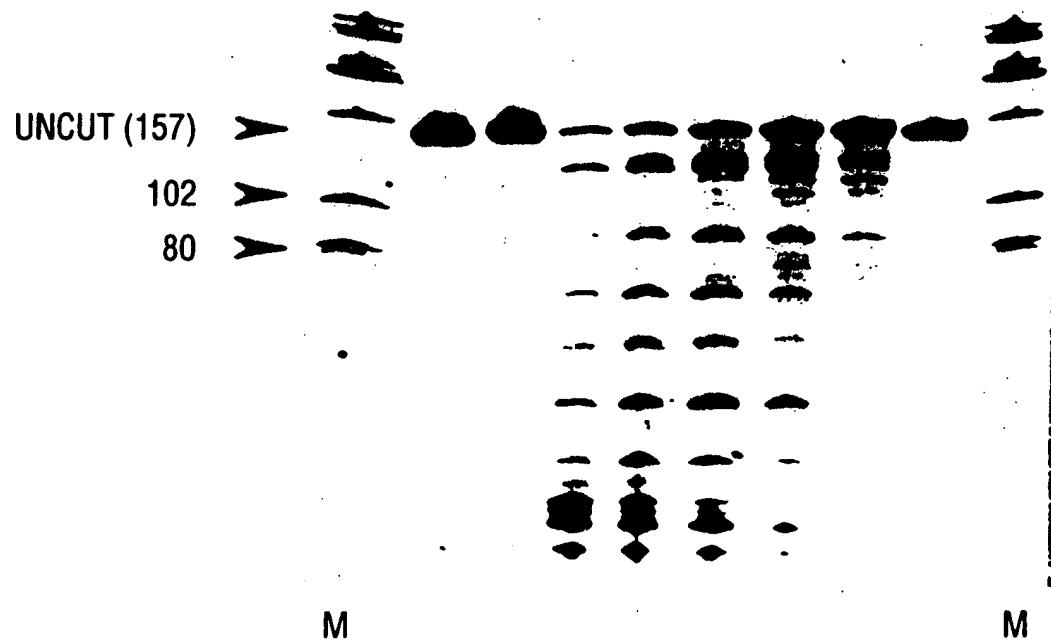


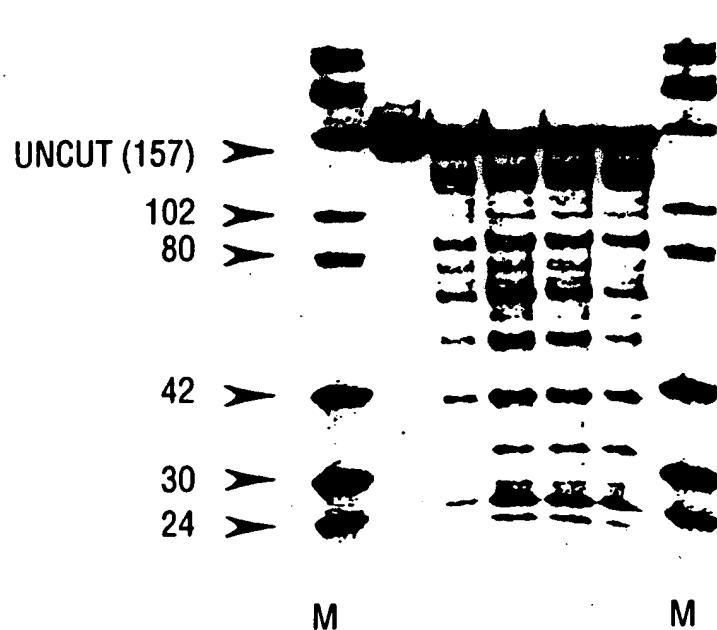
FIG. 36

TEMPERATURE (°C):	55	80	55	60	65	70	75	80
CLEAVASE™BN:	—	—	+	+	+	+	—	+



**FIG. 37**

CLEAVASE<sup>TM</sup>BN (ng): - 10 50 100 250



**FIG. 38**

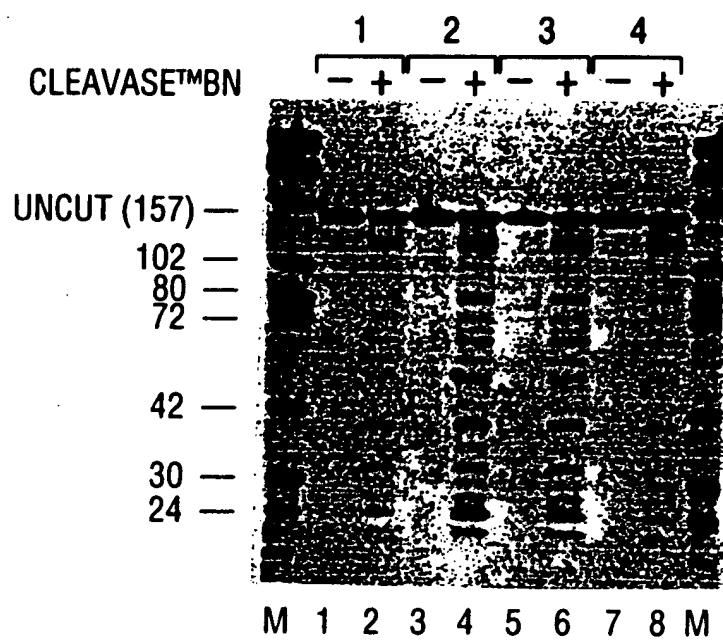


FIG. 39

STRAND	5' - BIOTIN SENSE STRAND				5' - FLUORESCIN ANTI-SENSE STRAND				
	WT	419	422	WT	419	422	WT	419	422
ssDNA									
250 <sup>ng</sup> BN	-	-	-	+	+	+	+	+	-
M	1	2	3	4	5	6	7	8	9
									10
									11
									12

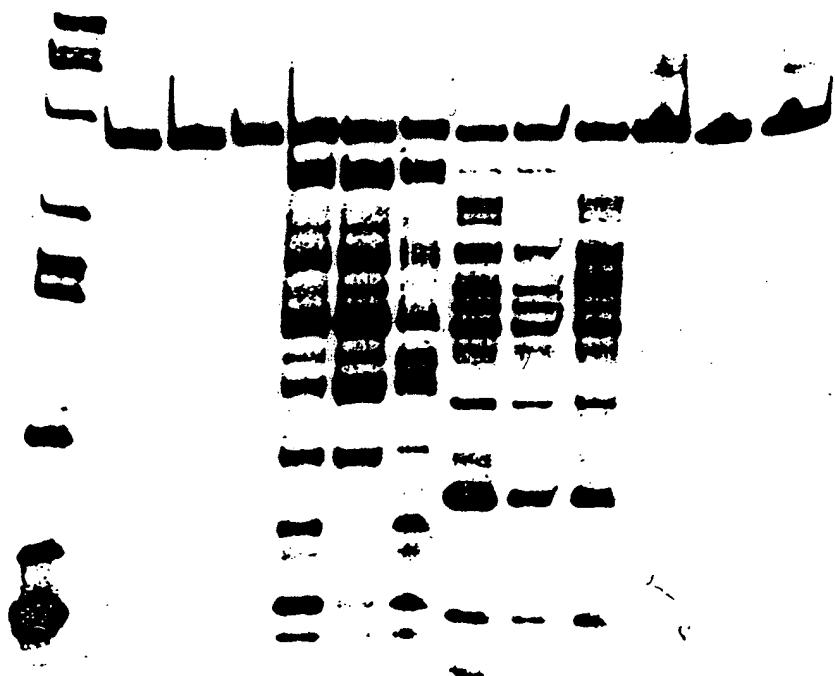
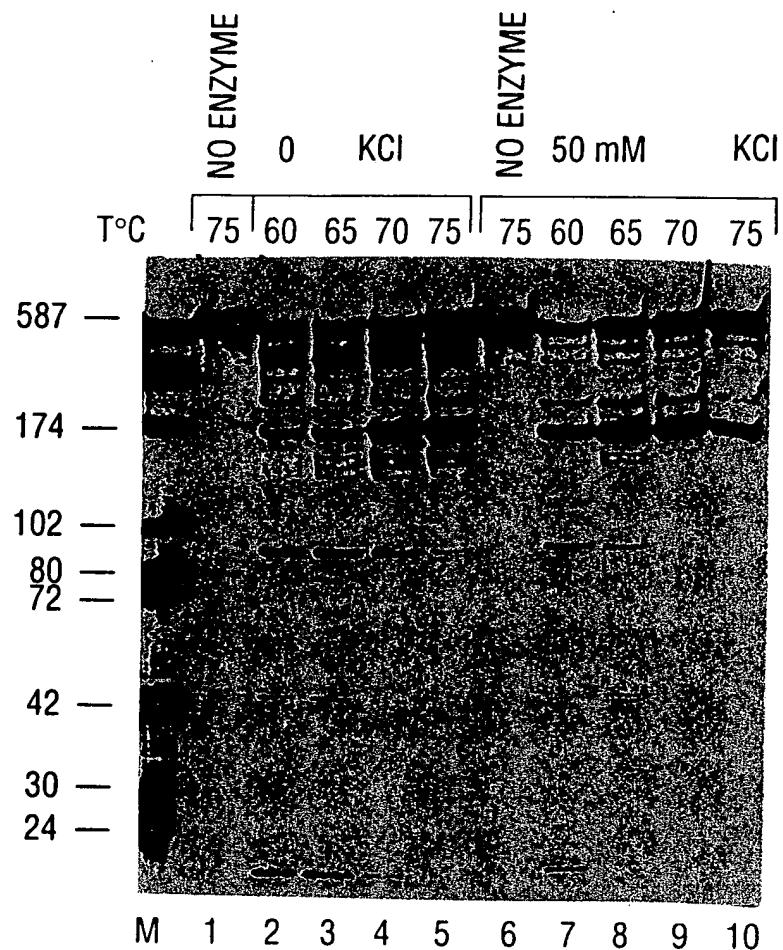
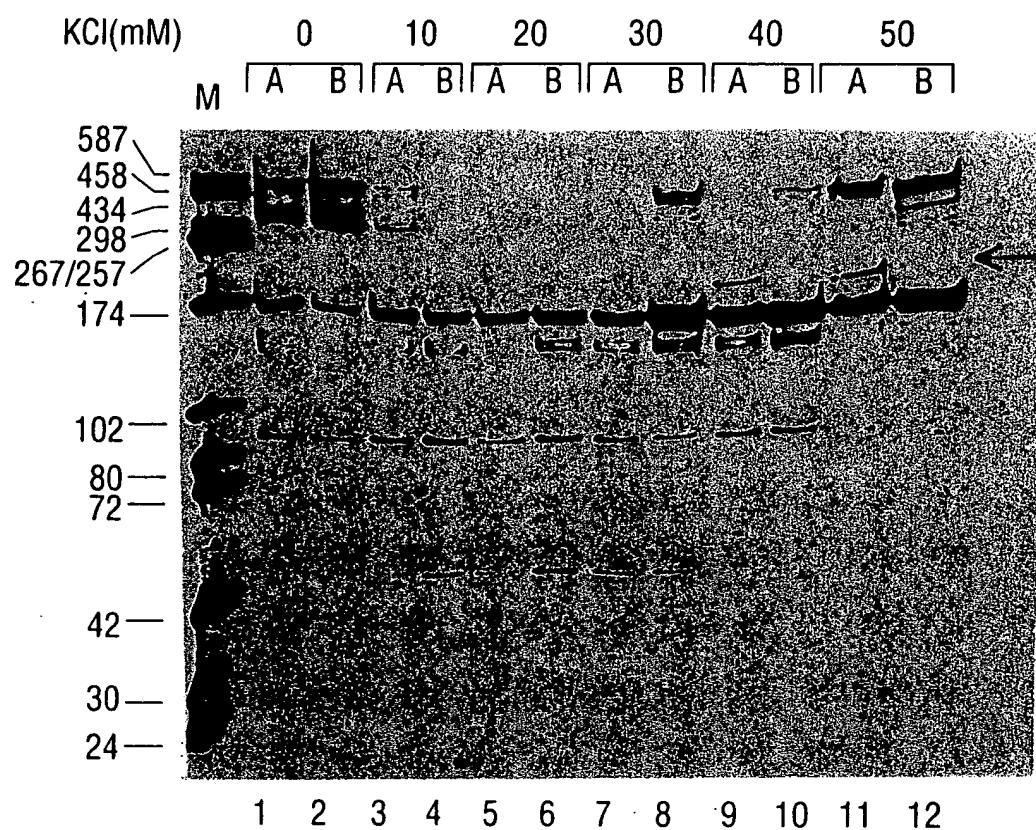


FIG. 40



**FIG. 41**



**FIG. 42**

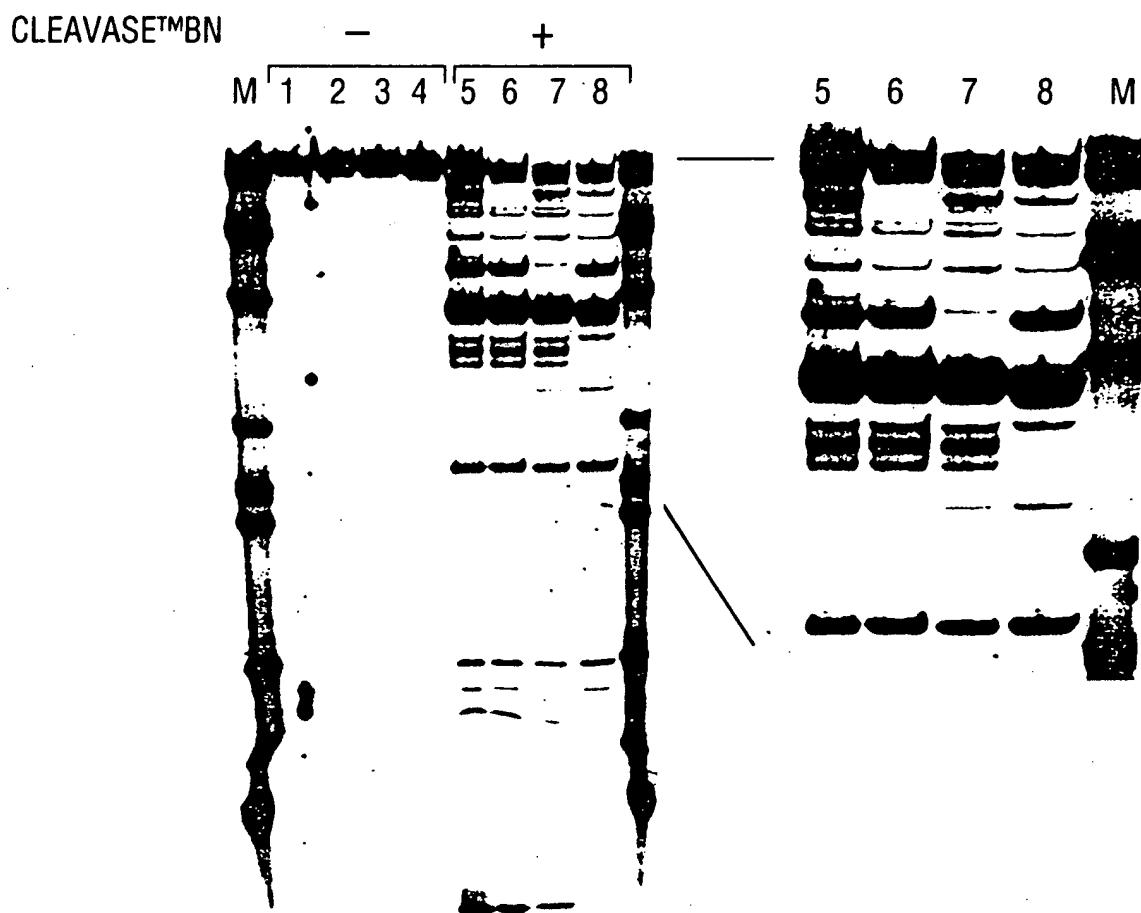


FIG. 43

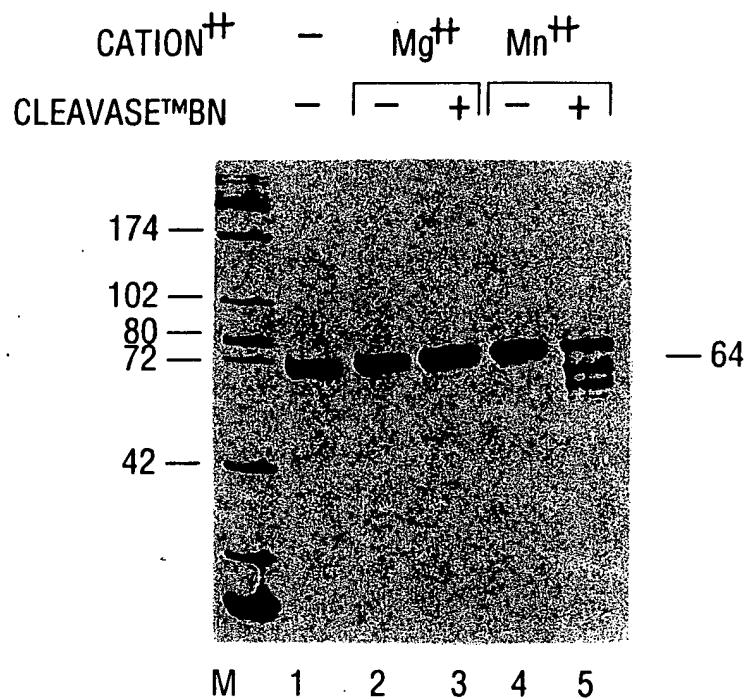


FIG. 44

"Replacement Sheet"

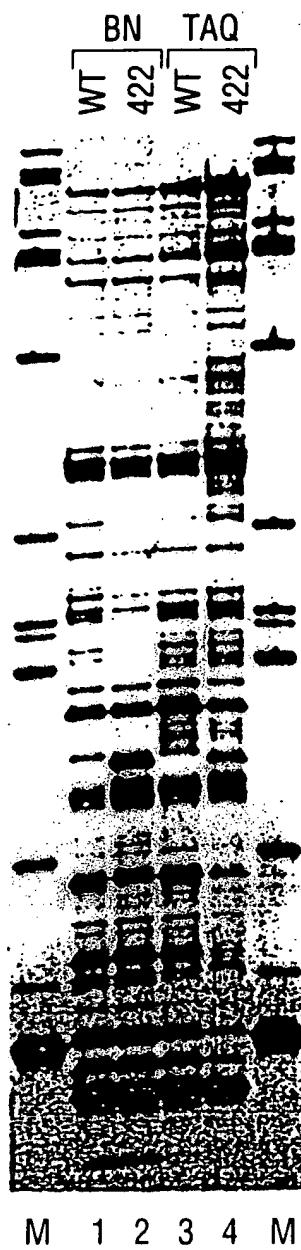


FIG. 45

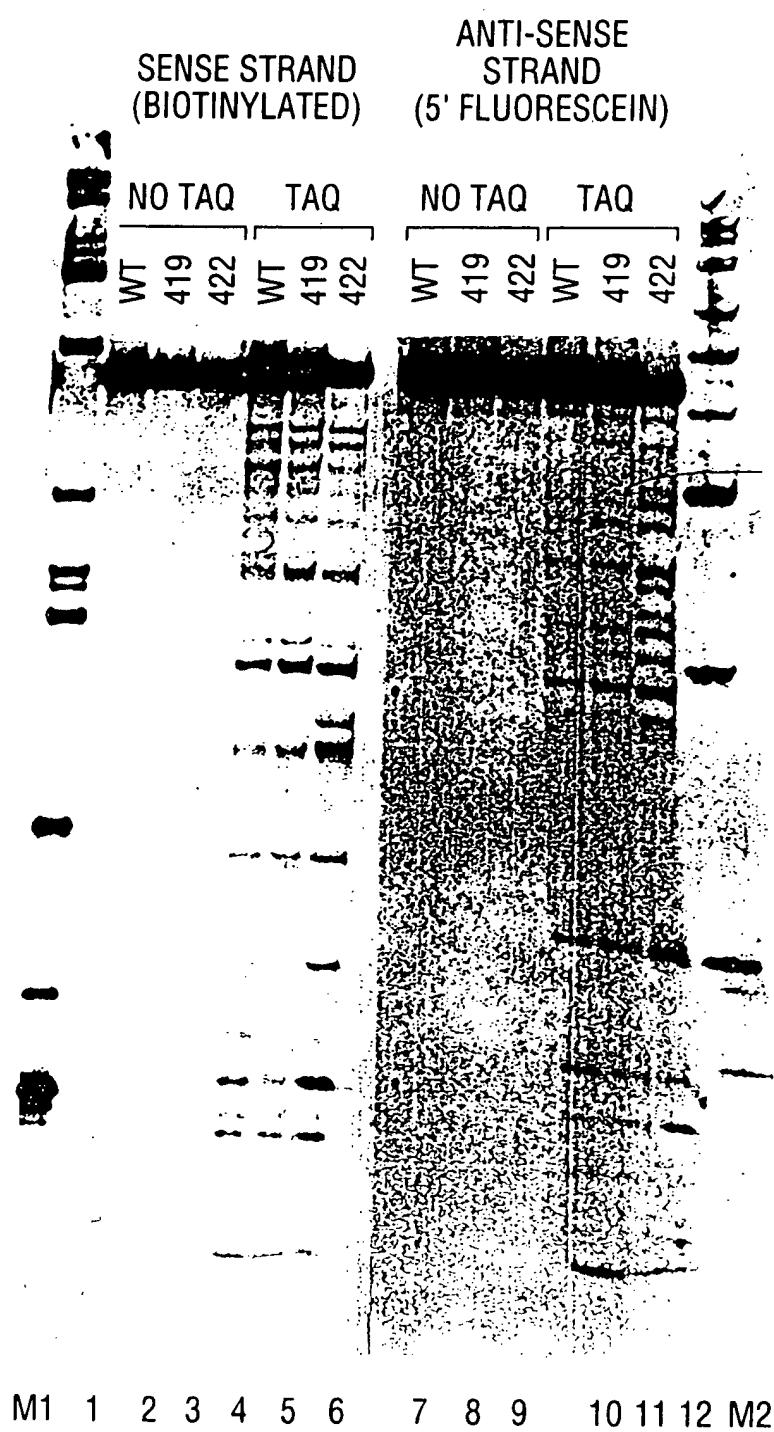
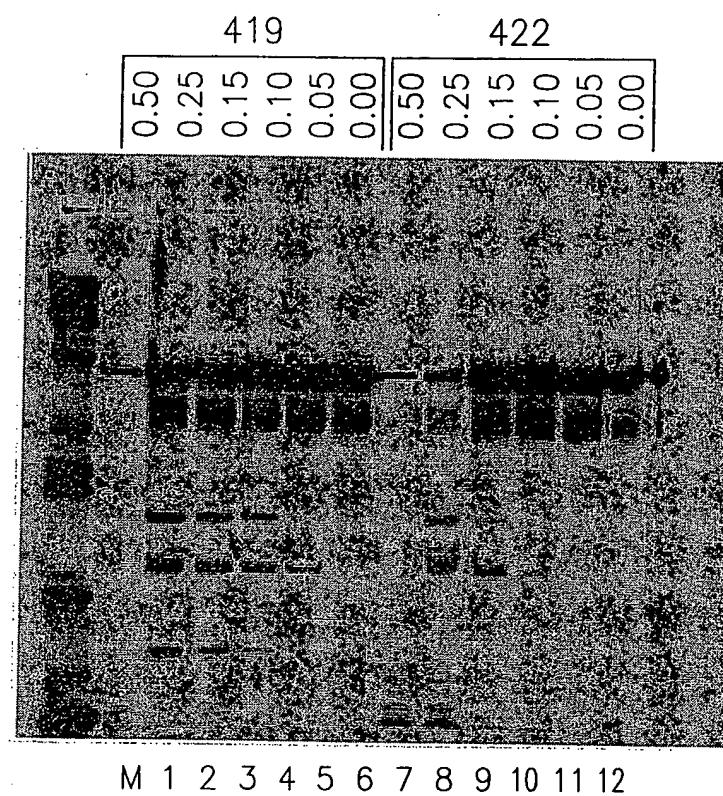


FIG. 46



**FIG. 47**

"Replacement Sheet"

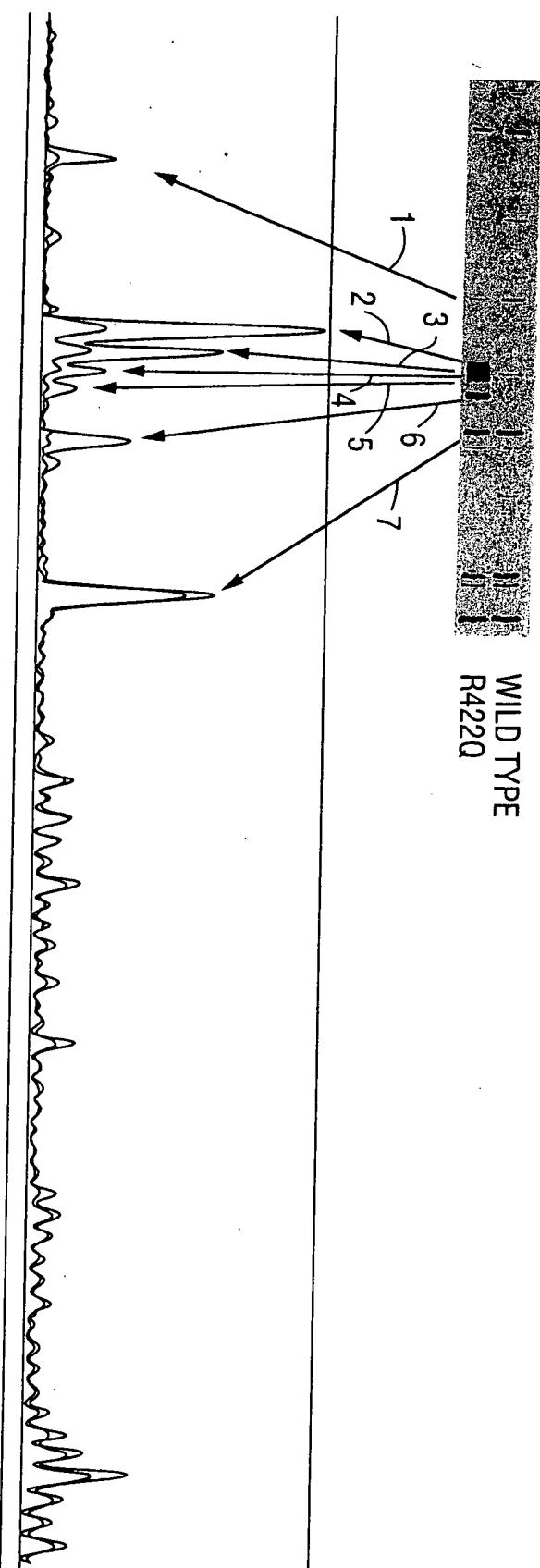


FIG. 48

L:100.8-1 (SEQ ID NO: 76)	5' GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAAGGGG 3' CCGACTGTTCTTCCTTGAAGGTGTTCCCC
L:46.16-10 (SEQ ID NO: 77)	5' GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAAGGGG 3' CCGACTGTTCTTCCTTGAAGGTGTTCCCC
L:46.16-12 (SEQ ID NO: 78)	5' GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAAGGGG 3' CCGACTGTTCTTCCTTGAAGGTGTTCCCC
L19.16-3 (SEQ ID NO: 79)	5' GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAAGGGG 3' CCGACTGTTCTTCCTTGAAGGTGTTCCCC
L:CEM/251 (SEQ ID NO: 80)	5' GGCTGACAAGAAGGAAACTCGCTGAAACAGCAGGGACTTTCCACAAAGGGG 3' CCGACTGTTCTTCCTTGAAGGTGTTCCCC
L:36.8-3 (SEQ ID NO: 81)	5' GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAAGGGG 3' CCGACTGTTCTTCCTTGAAGGTGTTCCCC

## "Replacement Sheet"

FIG. 49A

L.100.8-1  
(SEQ ID No: 76)

100  
ATGTTACGGGAGGTACTGGGGAGGAGCCGGTCCGGAACGCCCACTCTCT  
TACAATGCCCTCCATGACCCCTCCTCGCCAGCCCCCTTGGGTGAGAGA

L.46.16-10  
(SEQ ID No: 77)

ATGTTATGGGAGG-----AGCCGGTCCGGAACACCCACCTTTCT  
TACAATAACCCCTCC-----TCGGCCAGCCCCCTTGGGTGAAAGA

L.46.16-12  
(SEQ ID No: 78)

ATGTTACGGGAGGTACTGGGGAGGAGCCGGTCCGGAACGCCCACTTTCT  
TACAATGCCCTCC-----TCGGCCAGCCCCCTTGGGTGAAAGA

L.19.16-3  
(SEQ ID No: 19)

ATGTTACGGGAGGTACTGGGAAGGGAGCCGGTCCGGAACGCCCACTTTCT  
TACAATGCCCTCCATGACCCCTCCTCGCCAGCCCCCTTGGGTGAAAGA

L.CEM/251  
(SEQ ID No: 80)

ATGTTACGGGAGGTACTGGGAAGGGAGCCGGTCCGGAACGCCCACTTTCT  
TACAATGCCCTCC-----TCGGCCAGCCCCCTTGGGTGAAAGA

L.36.8-3  
(SEQ ID No: 81)

ATGTTACGGGAGGTACTGGGGAGGAGCCGGTCCGGAACGCCCACTTTCT  
TACAATGCCCTCCATGACCCCTCCTCGCCAGCCCCCTTGGGTGAGAGA

"Replacement Sheet"

**FIG. 49B**

150  
5' TGATGTATAAATATCACTGCATTTCGCTCTGTATTCAAGTCGGCTCTGCCGA  
3' ACTACATATTAGTGACGTAAAGCAGACATAAAGTCAGCGAGACGGCT

L. 46. 16-10  
5' TGGTGTATAAATATCACTGCATTTCGCTCTGTATTCAAGTCGGCTCTGCCGA  
3' ACCACATATTAGTGACGTAAAGCAGACATAAAGTCAGCGAGACGGCT

L. 46. 16-12  
5' TGATGTATAAATATCACTGCATTTCGCTCTGTATTCAAGTCGGCTCTGCCGA  
3' ACTACATATTAGTGACGTAAAGCAGACATAAAGTCAGCGAGACGGCT

L. 19. 16-3  
5' TGATGTATAAATATCACTGCATTTCGCTCTGTATTCAAGTCGGCTCTGCCGA  
3' ACTACATATTAGTGACGTAAAGCAGACATAAAGTCAGCGAGACGGCT

L. CEM/251  
5' TGATGTATAAATATCACTGCATTTCGCTCTGTATTCAAGTCGGCTCTGCCGA  
3' ACTACATATTAGTGACGTAAAGCAGACATAAAGTCAGCGAGACGGCT

L. 36. 8-3  
5' TGATGTATAAATATCACTGCATTTCGCTCTGTATTCAAGTCGGCTCTGCCGA  
3' ACTACATATTAGTGACGTAAAGCAGACATAAAGTCAGCGAGACGGCT

**FIG. 49C**

L.100.8-1

200  
GAGGCTGGCAGATTGAGGCCCTGGGAGGGTTCTCCAGGCACTAGCAGGTAG  
CTCCGACCCGTCTAACTCGGGACCCCTCCAAAGAGGAGGTGATCGTGTGATCGTCCATC

L.46.16-10

GAGGCTGGCAGATTGAGGCCCTGGGAGGGTTCTCCAGGCACTAGCAGGTAG  
CTCCGACCCGTCTAACTCGGGACCCCTCCAAAGAGGAGGTGATCGTGTGATCGTCCATC

L.46.16-12

GAGGCTGGCAGATTGAGGCCCTGGGAGGGTTCTCCAGGCACTAGCAGGTAG  
CTCCGACCCGTCTAACTCGGGACCCCTCCAAAGAGGAGGTGATCGTGTGATCGTCCATC

L.19.16-3

GAGGCTGGCAGATTGAGGCCCTGGGAGGGTTCTCCAGGCACTAGCAGGTAG  
CTCCGACCCGTCTAACTCGGGACCCCTCCAAAGAGGAGGTGATCGTGTGATCGTCCATC

L.CEM/251

GAGGCTGGCAGATTGAGGCCCTGGGAGGGTTCTCCAGGCACTAGCAGGTAG  
CTCCGACCCGTCTAACTCGGGACCCCTCCAAAGAGGAGGTGATCGTGTGATCGTCCATC

L.36.8-3

GAGGCTGGCAGATTGAGGCCCTAGGAGGGTTCTCCAGGCACTAGCAGGTAG  
CTCCGACCCGTCTAACTCGGGATCCAAAGAGGAGGTGATCGTGTGATCGTCCATC

"Replacement Sheet"

**FIG. 49D**

L. 100. 8 -1 5' AGCCTGGTGTCCCCCTGCTAGACTCTCACCAAGGCACCTTGGGG  
(SEQ ID NO: 76) 3' TCGGACCCACAAGGACCATCTGAGAGTGGTCAACGACCC

L. 46.16-10 5' AGCCTGGTGTCCCCCTGCTAGACTCTCACCAAGGCACCTTGGGG  
(SEQ ID NO: 77) 3' TCGGACCCACAAGGACCATCTGAGAGTGGTCAACGACCC

L. 46.16-12 5' AGCCTGGTGTCCCCCTGCTAGACTCTCACCAAGGCACCTTGGGG  
(SEQ ID NO: 78) 3' TCGGACCCACAAGGACCATCTGAGAGTGGTCAACGACCC

L. 19.16-3 5' AGCCTGGTGTCCCCCTGCTAGACTCTCACCAAGGCACCTTGGGG  
(SEQ ID NO: 79) 3' TCGGACCCACAAGGACCATCTGAGAGTGGTCAACGACCC

L. CEM/251 5' AGCCTGGTGTCCCCCTGCTAGACTCTCACCAAGGCACCTTGGGG  
(SEQ ID NO: 80) 3' TCGGACCCACAAGGACCATCTGAGAGTGGTCAACGACCC

L. 36.8-3 5' AGCCTGAGTGGTCCCCCTGCTAAACTCACCAAGGCACCTTGGGG  
(SEQ ID NO: 81) 3' TCGGACTCACAAAGGACGATTGAGAGTGGTCAACGACCC

HAIRPIN

**FIG. 49E**

300

L. 100. 8 -1  
(SEQ ID No: 76)

L. 46.16-10  
(SEQ ID No: 77)

L. 46.16-12  
(SEQ ID No: 78)

L. 19.16-3  
(SEQ ID No: 79)

L. CEM/251  
(SEQ ID No: 80)

L. 36.8-3  
(SEQ ID No: 81)

CAGAGTGGCTCCACGGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
GTCTCAACGGTGGCAACGAATTTCGAGAAGTTCTGACGGC

CAGAGTGGCTCCACGGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
GTCTCAACGGAGGTGGCAACGAATTTCGAGAAGTTCTGACGGC

CAGAGTGGCTCCACGGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
GTCTCAACGGAGGTGGCAACGAATTTCGAGAAGTTCTGACGGC

CAGAGTGGCTCCACGGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
GTCTCAACGGAGGTGGCAACGAATTTCGAGAAGTTCTGACGGC

CAGAGTGGCTCCACGGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
GTCTCAACGGAGGTGGCAACGAATTTCGAGAAGTTCTGACGGC

CAGAGGCGCTCCACGGCTTGGCTTAAAGACCTCTTCAATAAAGCTGCC  
GTCTCGCGAGGTGGCAACGAATTTCGAGAAGTTCTGACGGC

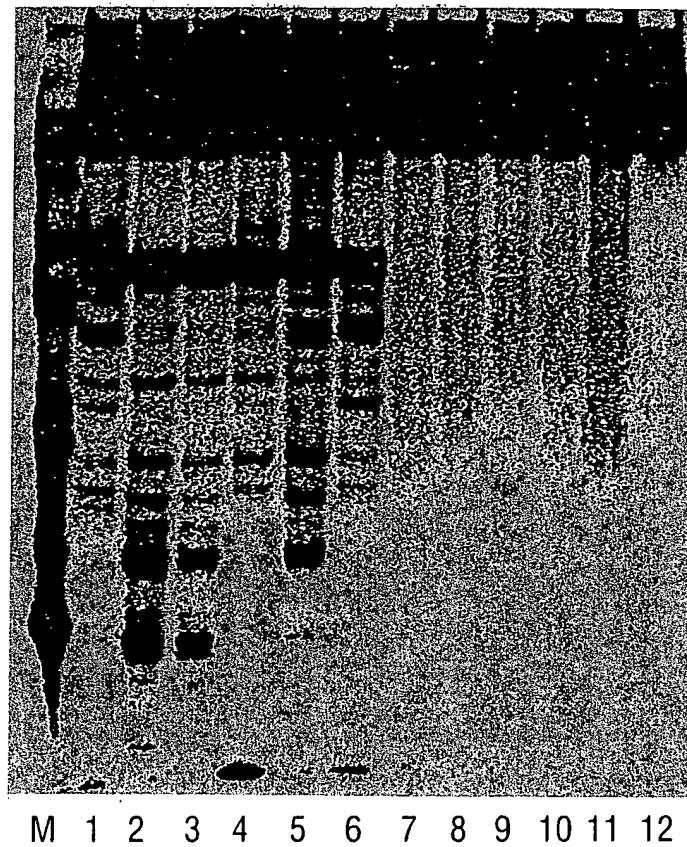
HAIRPIN

FIG. 49F

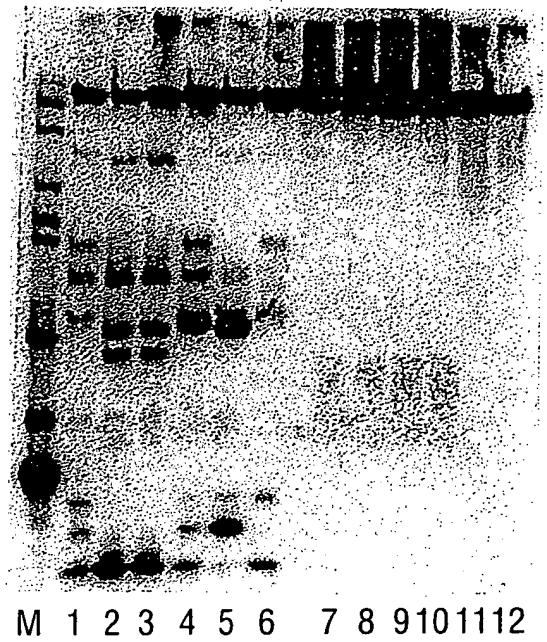
L. 100. 8-1	5' ATT TTAGAAGTAGGCCAGTGTGTTCCCATCTCCTAGCCCCGCCCCCTG 3' TAAAATCTTCATCCGGTACACACAAGGGTAGAGGGATCGGGGGAC	5' ATT TTAGAAGTAAGCCAGTGTGTTCCCATCTCCTAGCCCCGCCCCCTG 3' TAAAATCTTCATCCGGTACACACAAGGGTAGAGGGATCGGGGGAC	5' ATT TTAGAAGTAAGGCTAGTGTGTTCCCATCTCCTAGCCCCGCCCCCTG 3' TAAAATCTTCATCCGGTACACACAAGGGTAGAGGGATCGGGGGAC	5' ATT TTAGAAGTAAGGCTAGTGTGTTCCCATCTCCTAGCCCCGCCCCCTG 3' TAAAATCTTCATCCGGTACACACAAGGGTAGAGGGATCGGGGGAC	5' ATT TTAGAAGTAGGCCAGTGTGTTCCCATCTCCTAGCCCCGCCCCCTG 3' TAAAATCTTCATCCGGTACACACAAGGGTAGAGGGATCGGGGGAC
L. 46. 16-10					
L. 46. 16-12					
L. 19. 16-3					
L. CEM/251					
L. 36. 8-3					

## "Replacement Sheet"

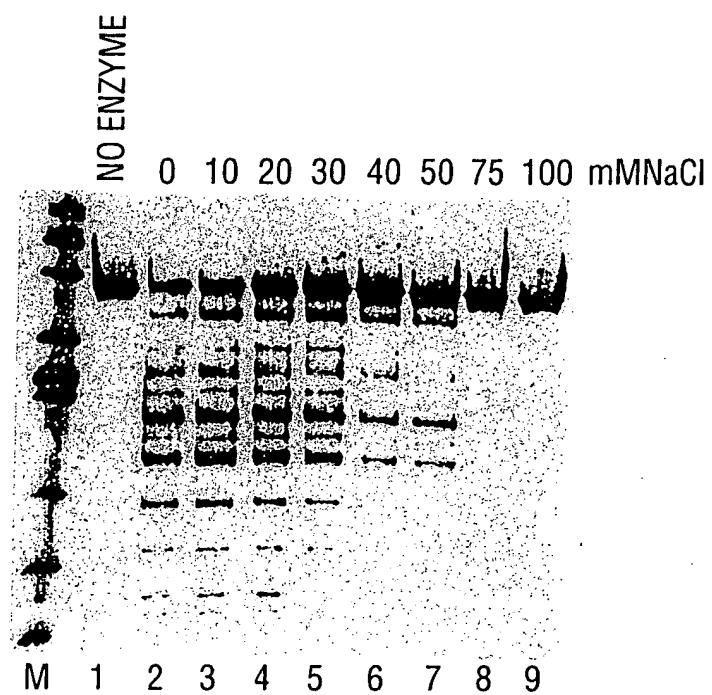
FIG. 49G



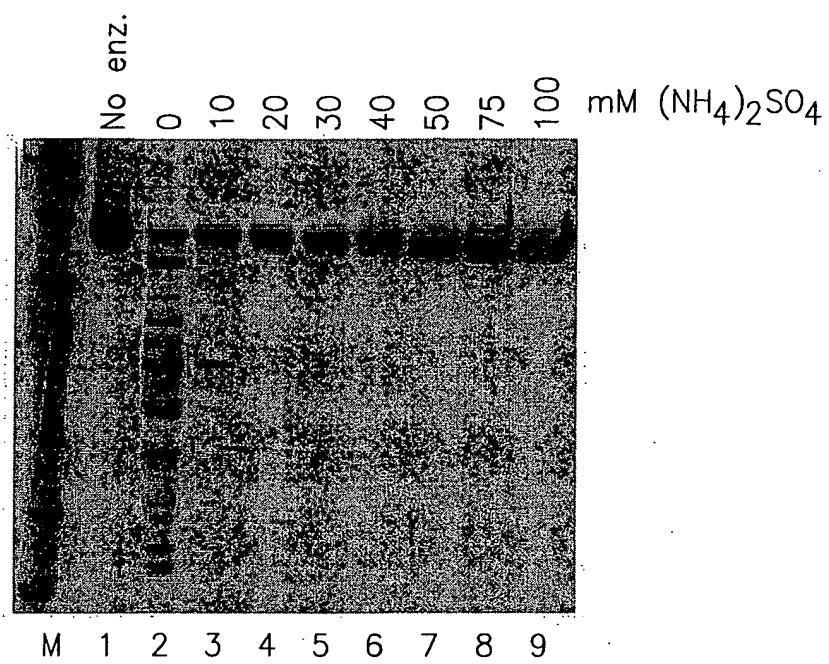
**FIG. 50**



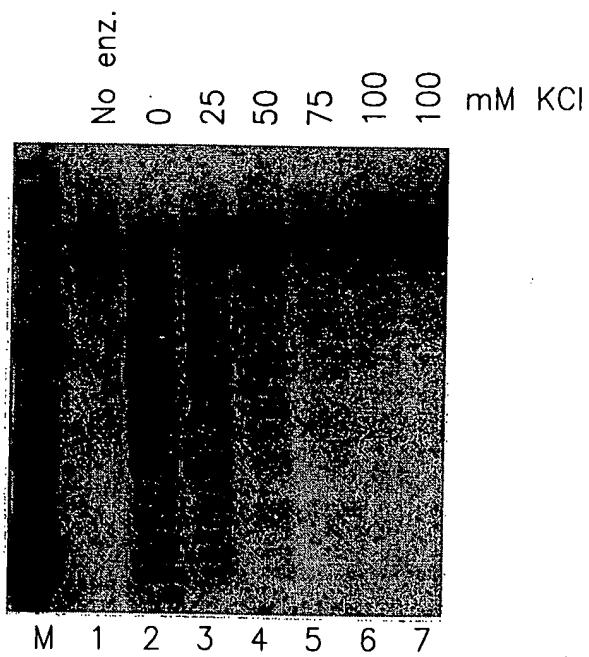
**FIG. 51**



**FIG. 52**



**FIG. 53**



**FIG. 54**

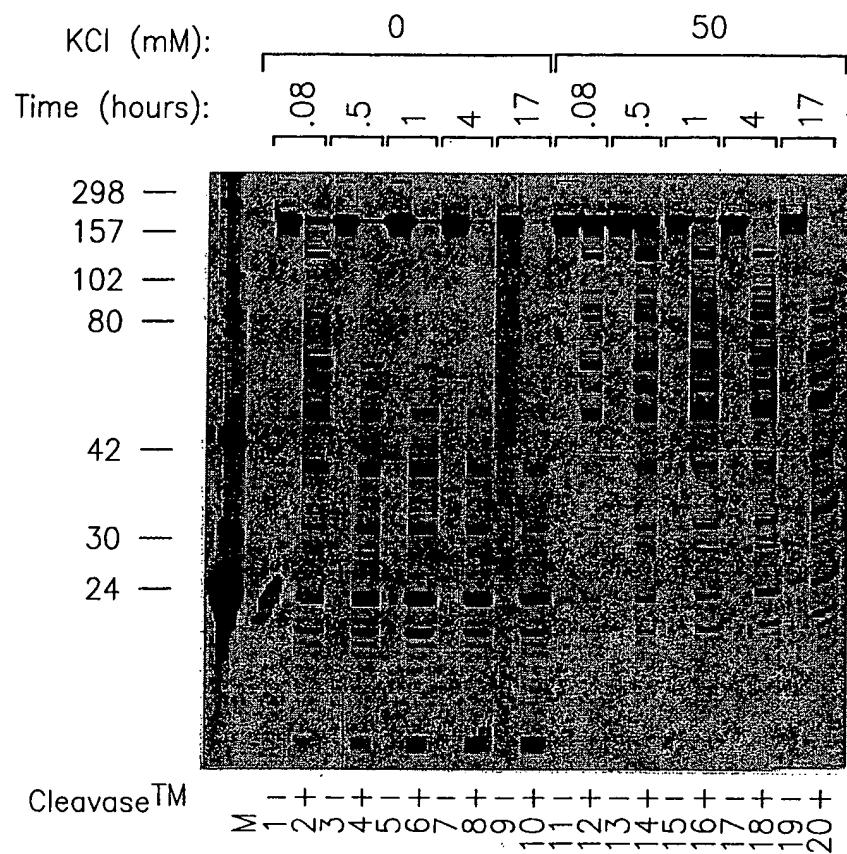
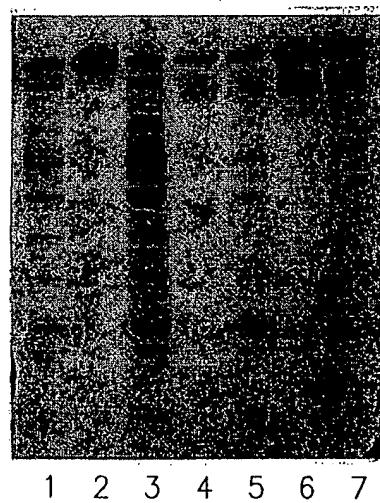
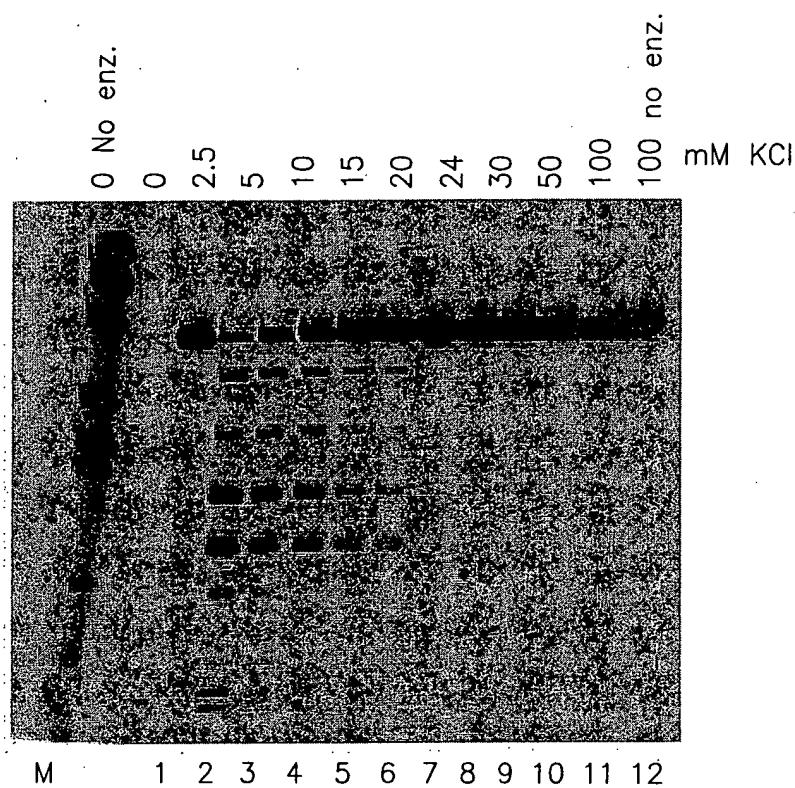


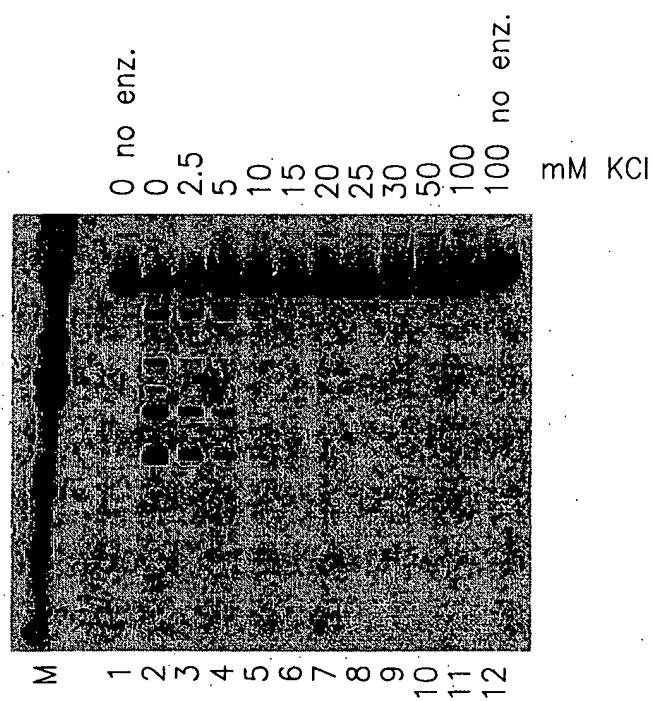
FIG. 55



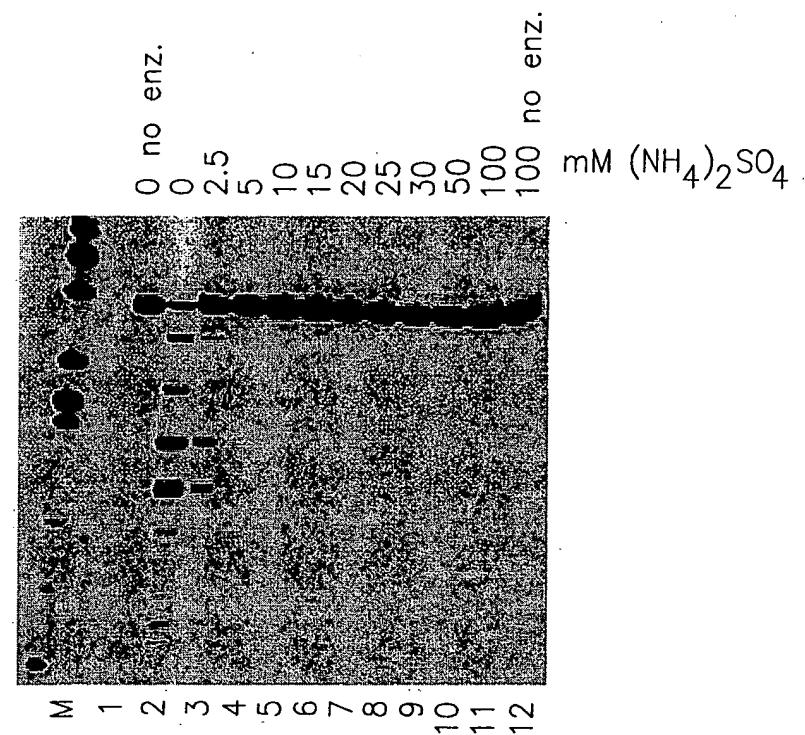
**FIG. 56**



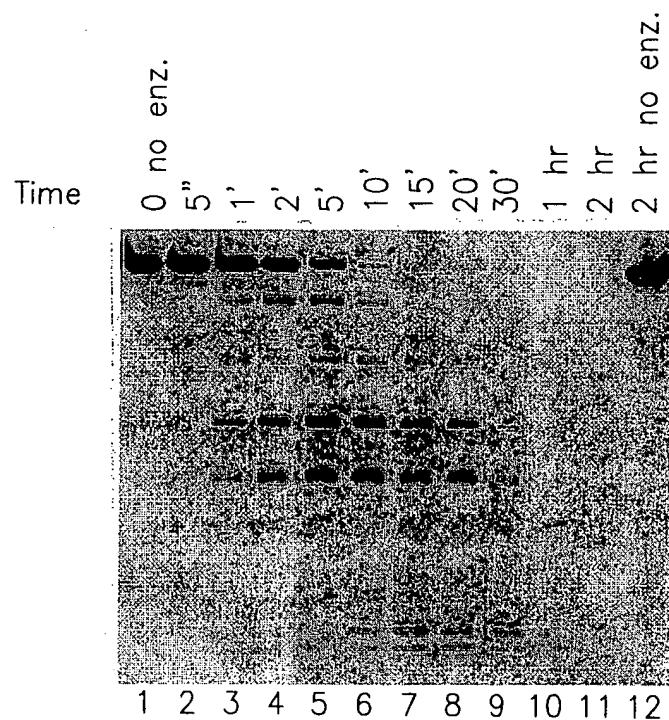
**FIG. 57**



**FIG. 58**

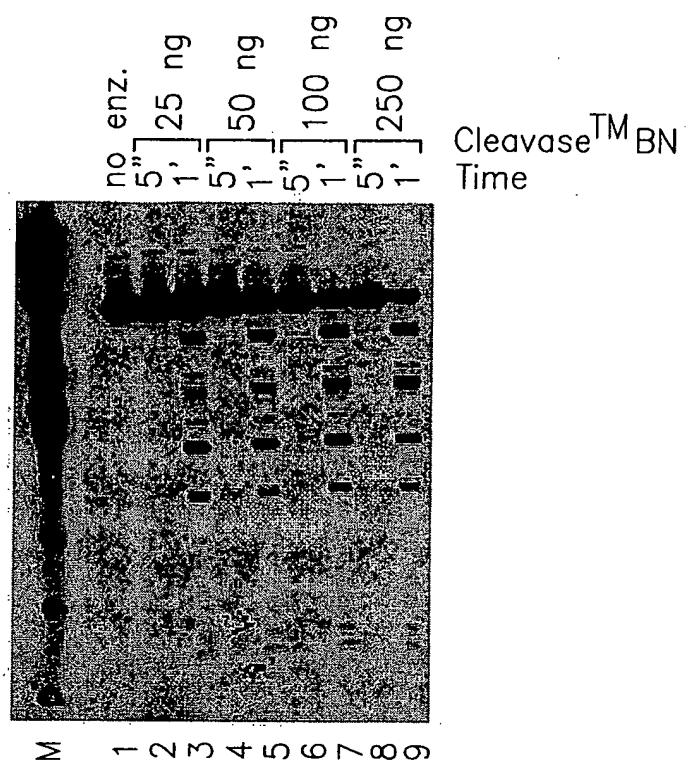


**FIG. 59**



**FIG. 60**

"Replacement Sheet"



**FIG. 61**

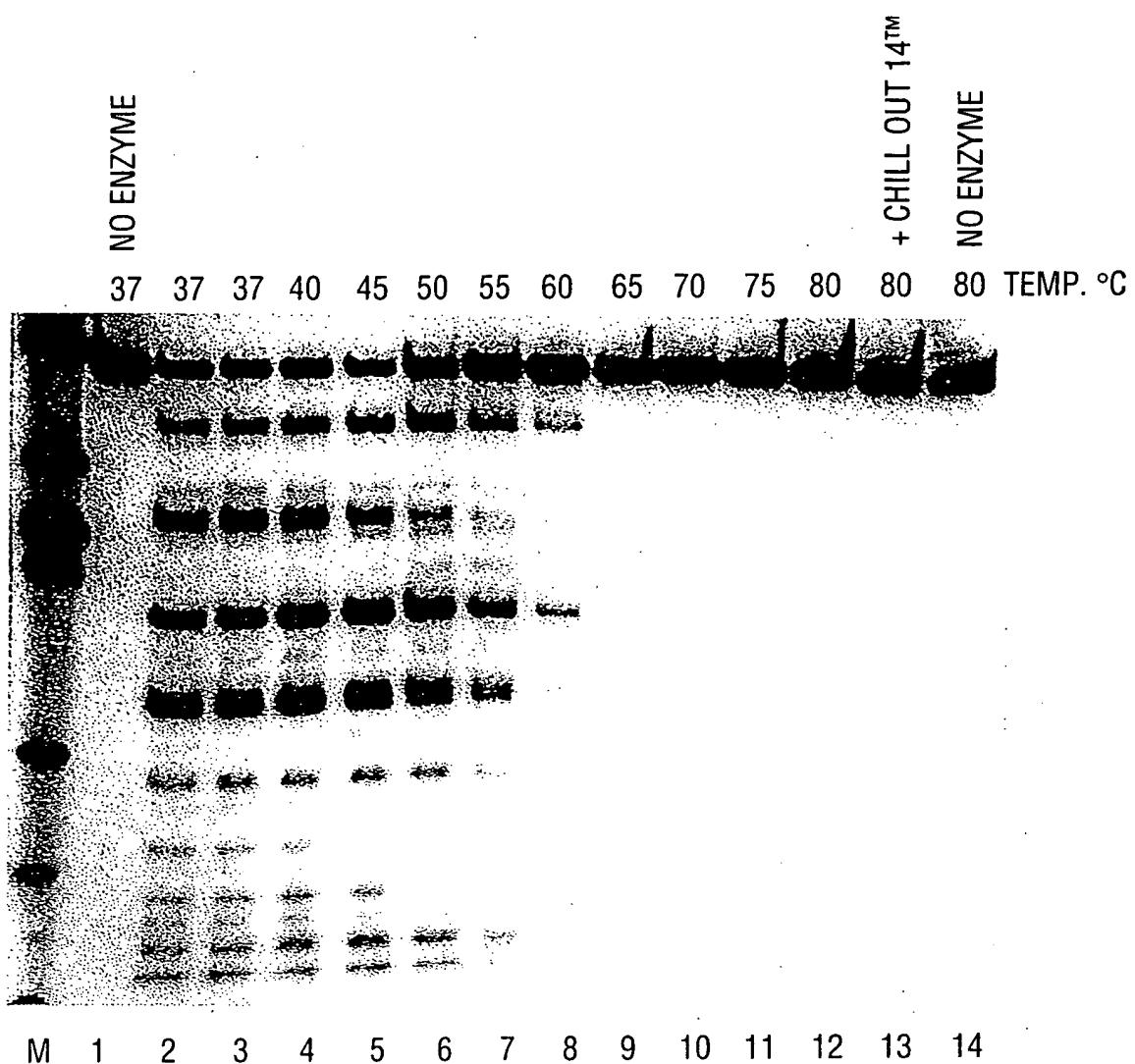
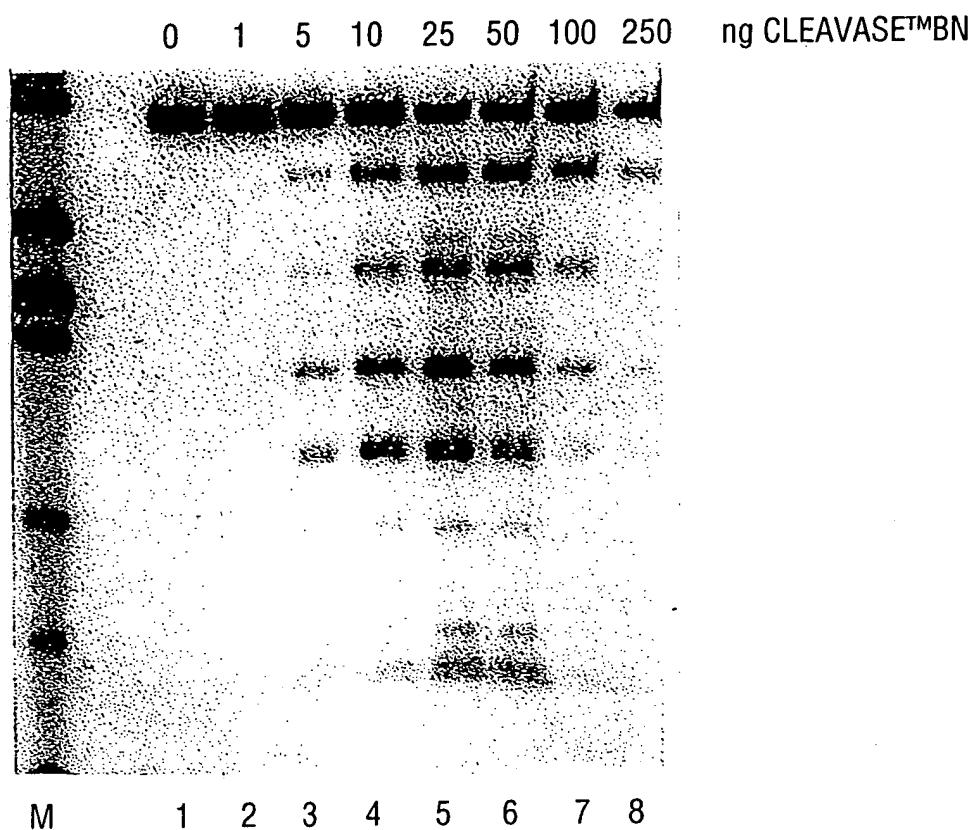


FIG. 62



**FIG. 63**

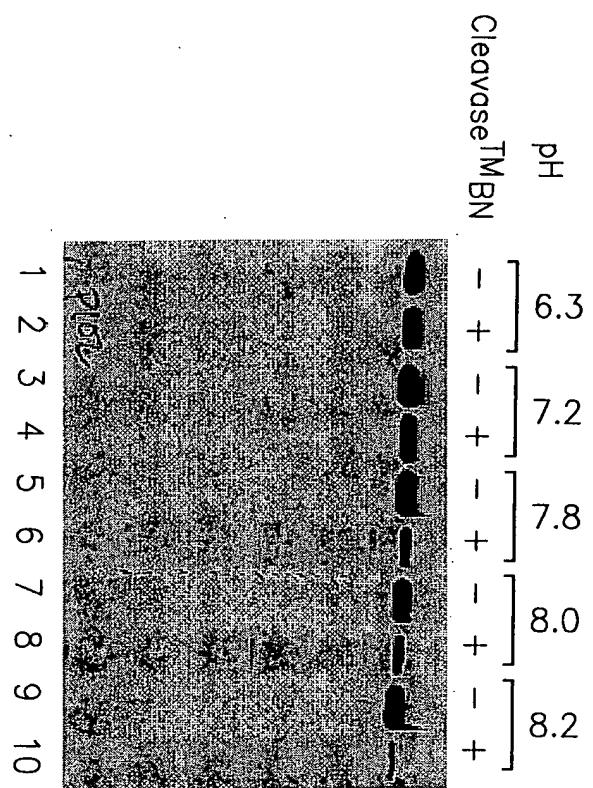


FIG. 64A

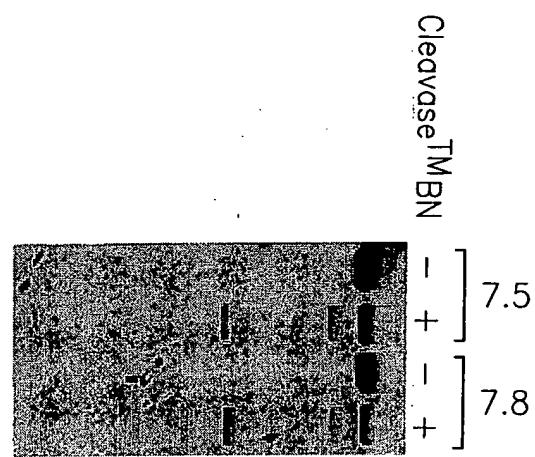
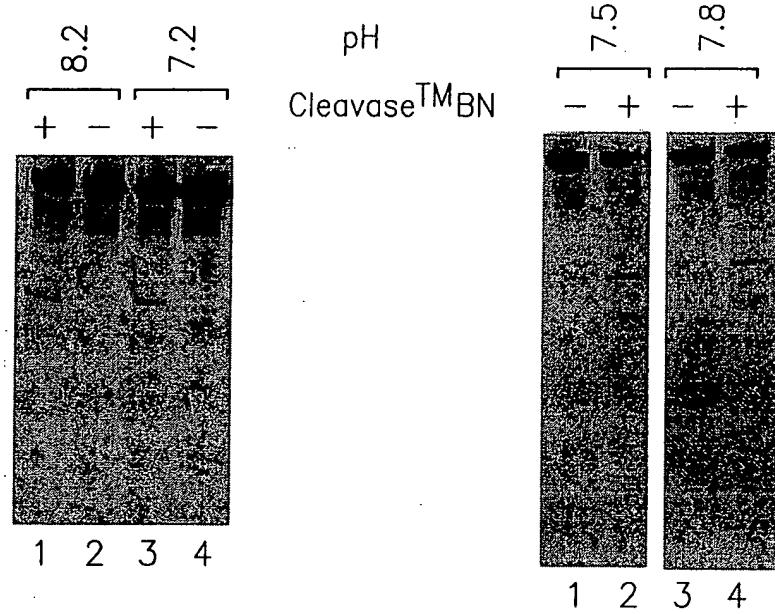
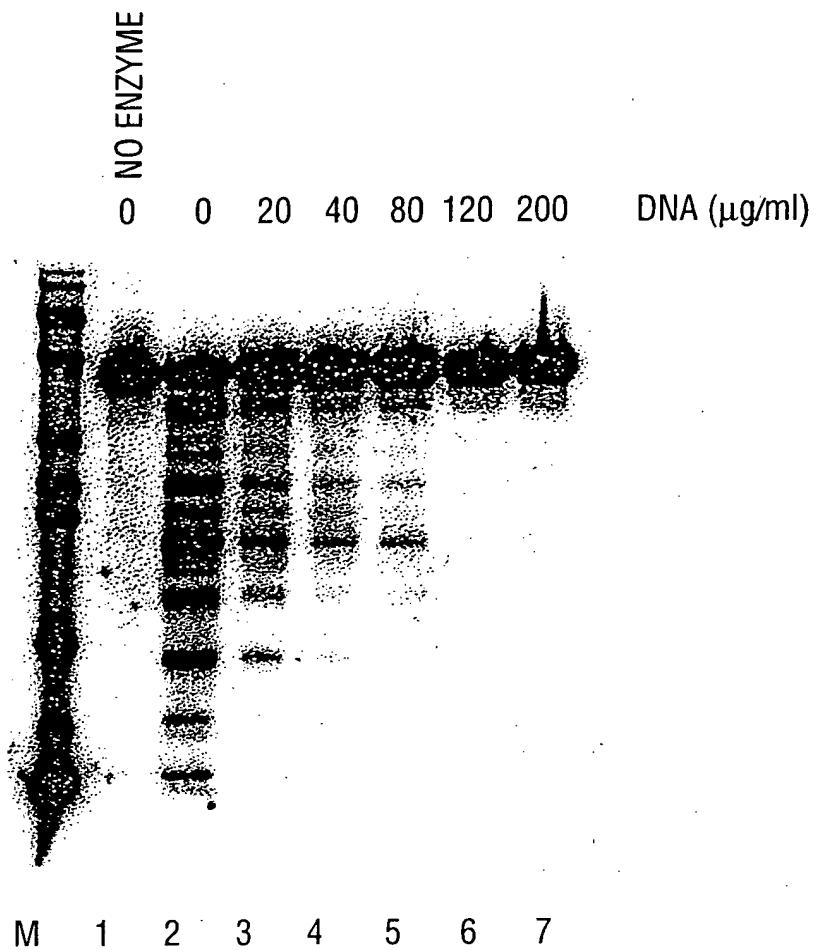


FIG. 64B

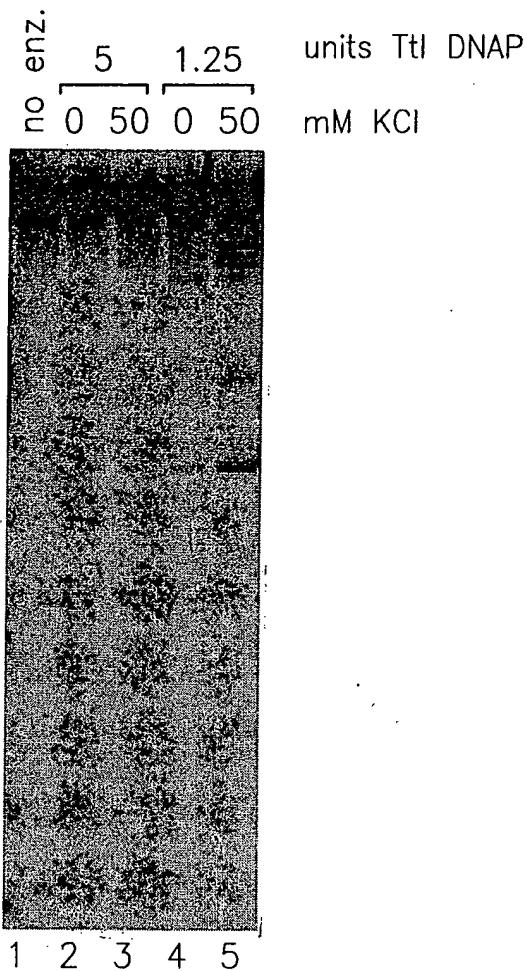


**FIG. 65A**

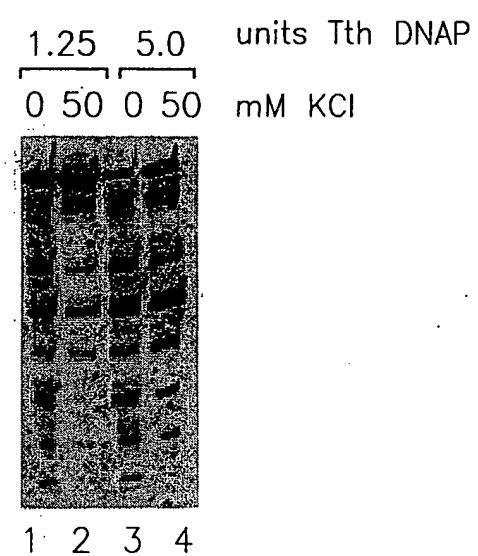
**FIG. 65B**



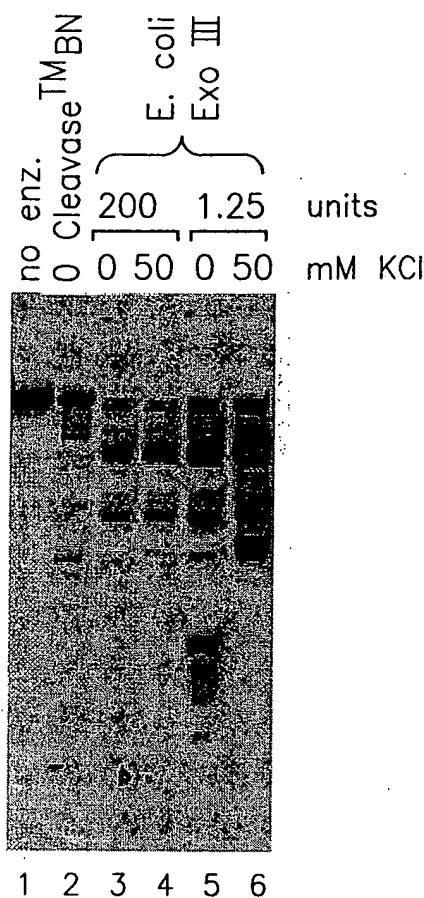
**FIG. 66**



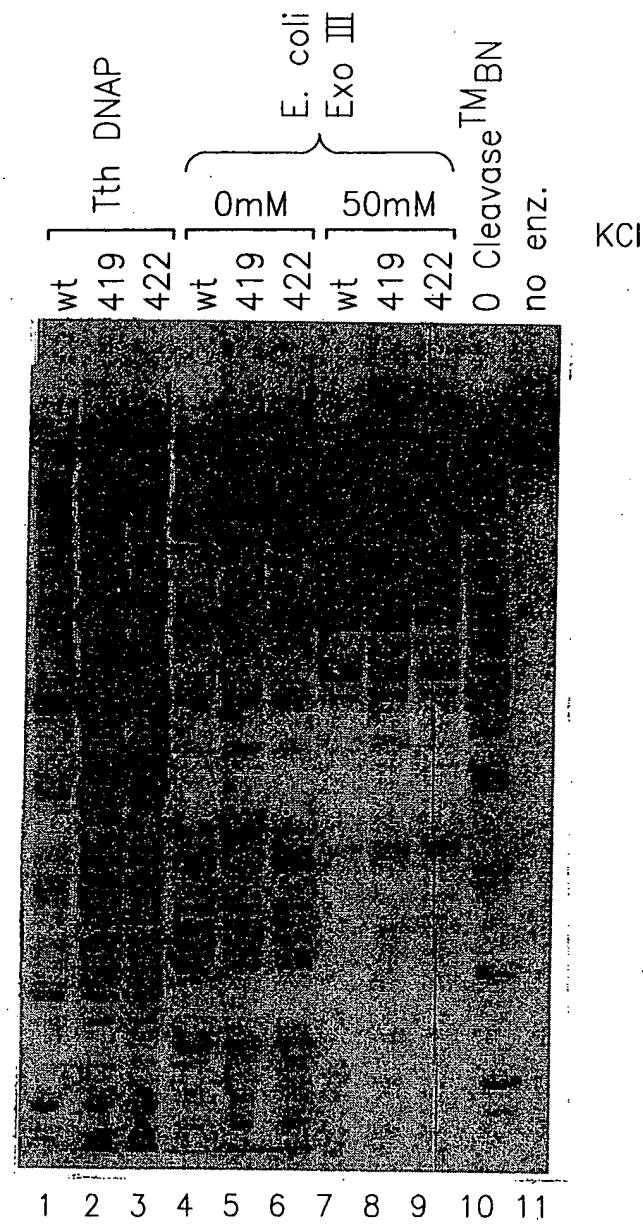
**FIG. 67**



**FIG. 68**

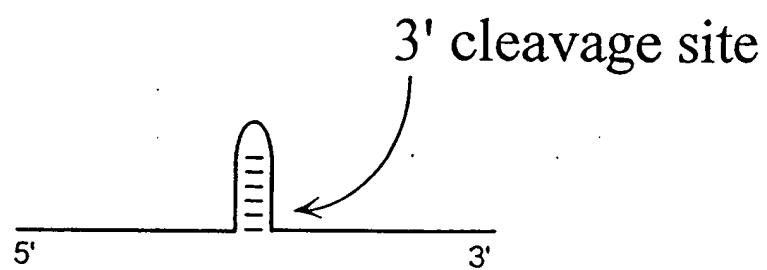
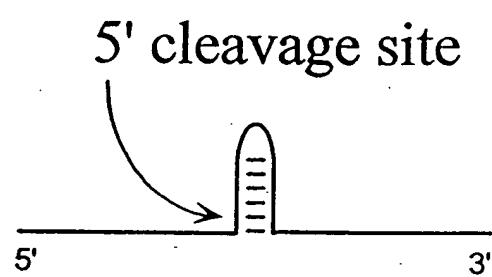


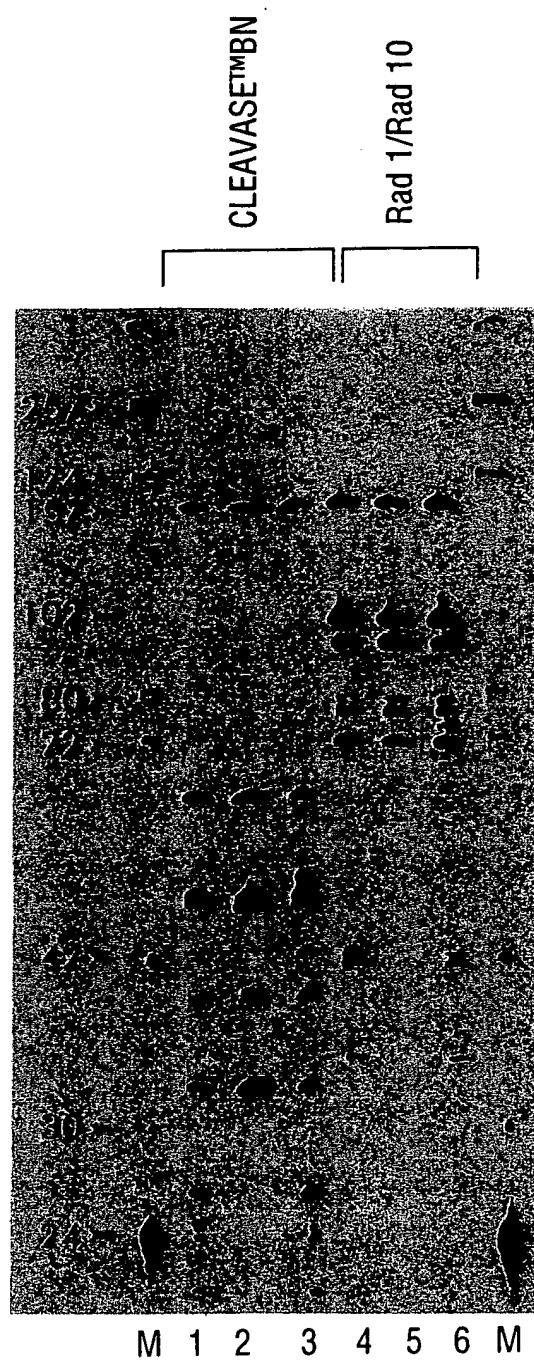
**FIG. 69**



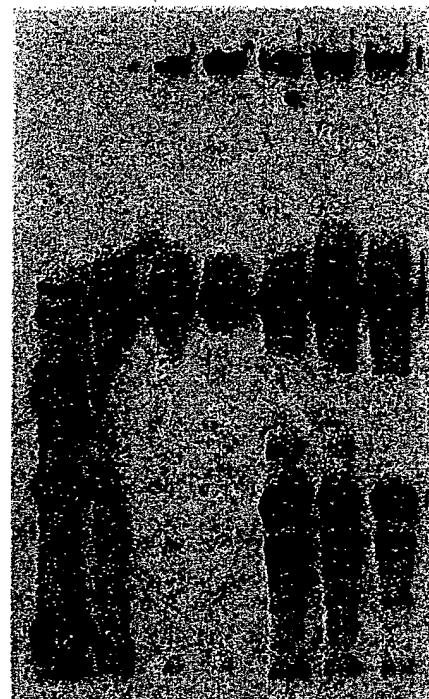
**FIG. 70**

**FIG. 71**





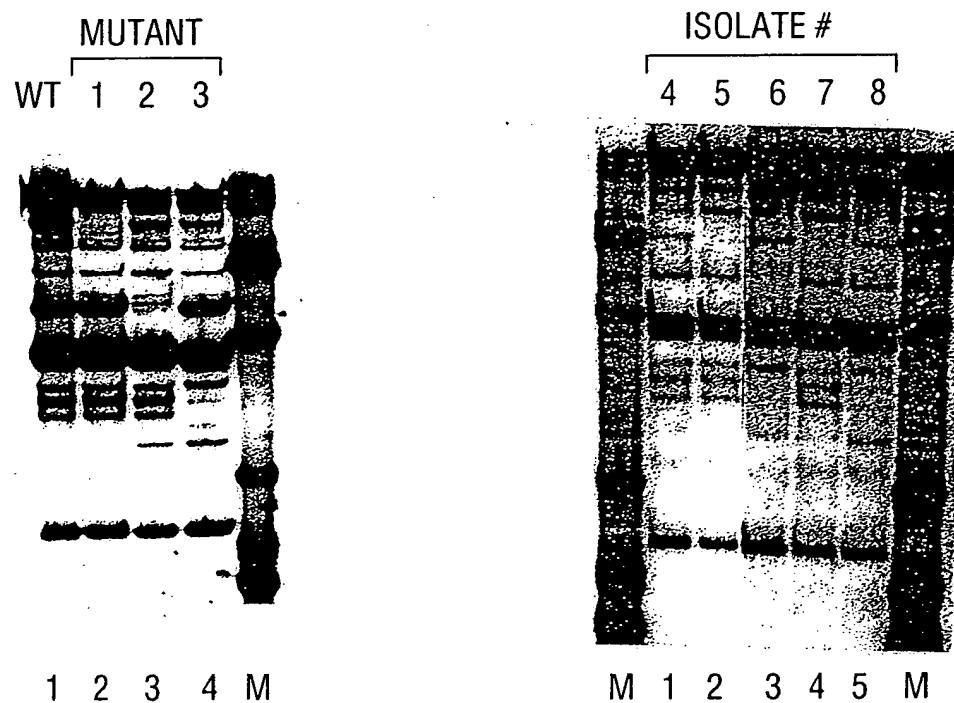
**FIG. 72**



174

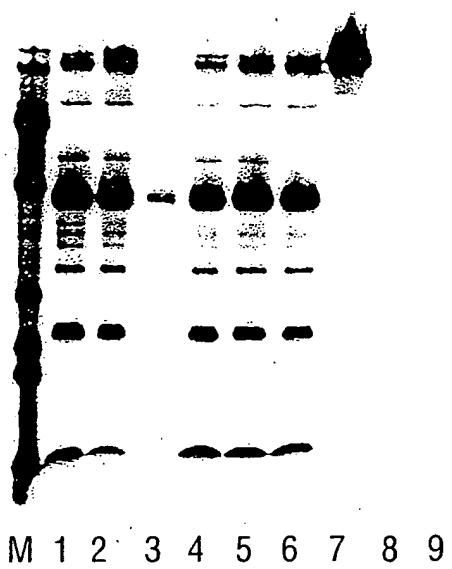
M 1 2 3 4 5 6

**FIG. 73**



**FIG. 74A**

**FIG. 74B**



**FIG. 75**

% OF TOTAL  
MUTATIONS

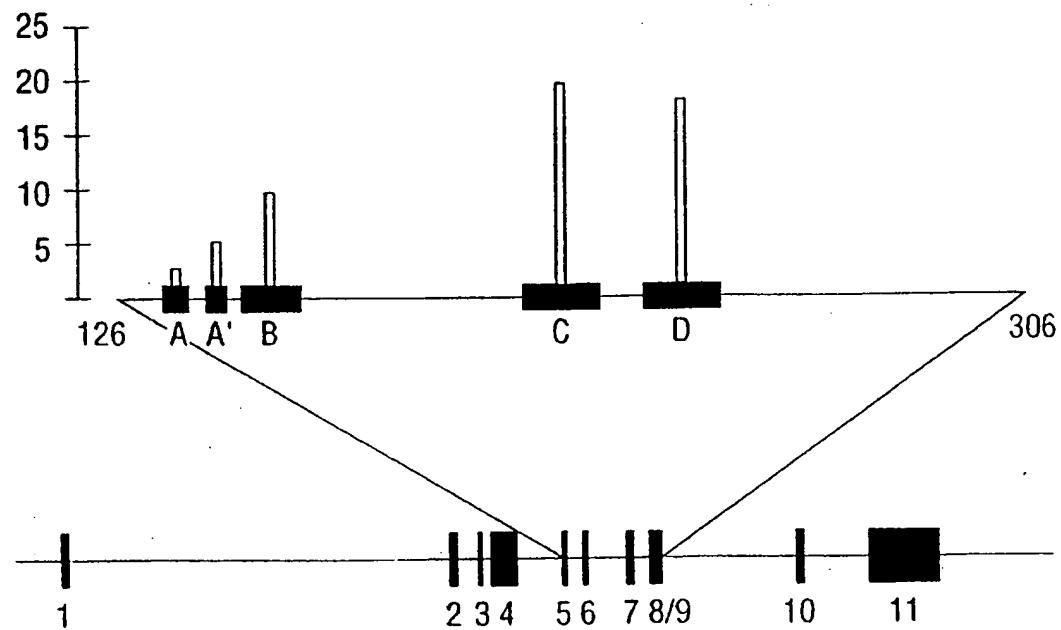


FIG. 76

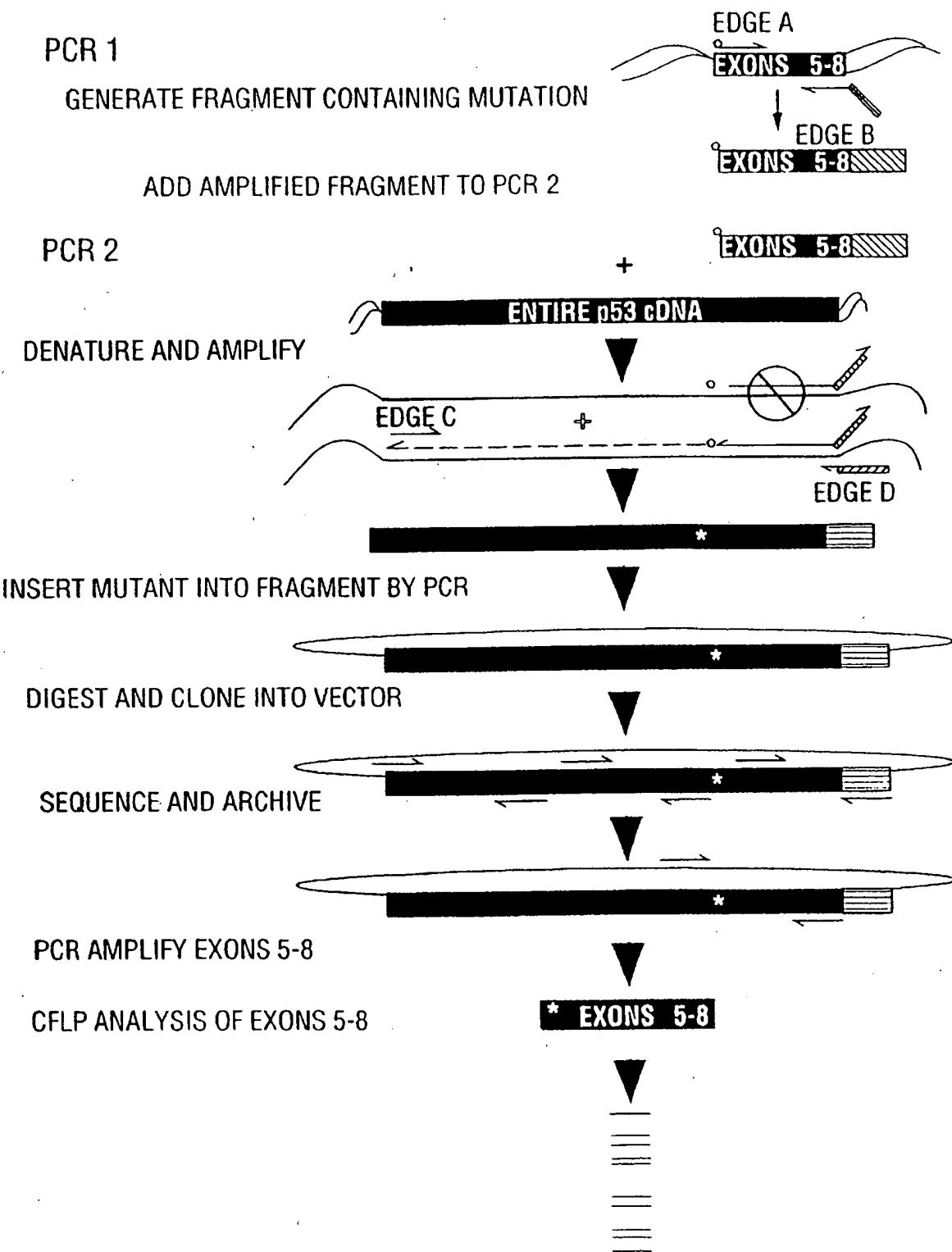
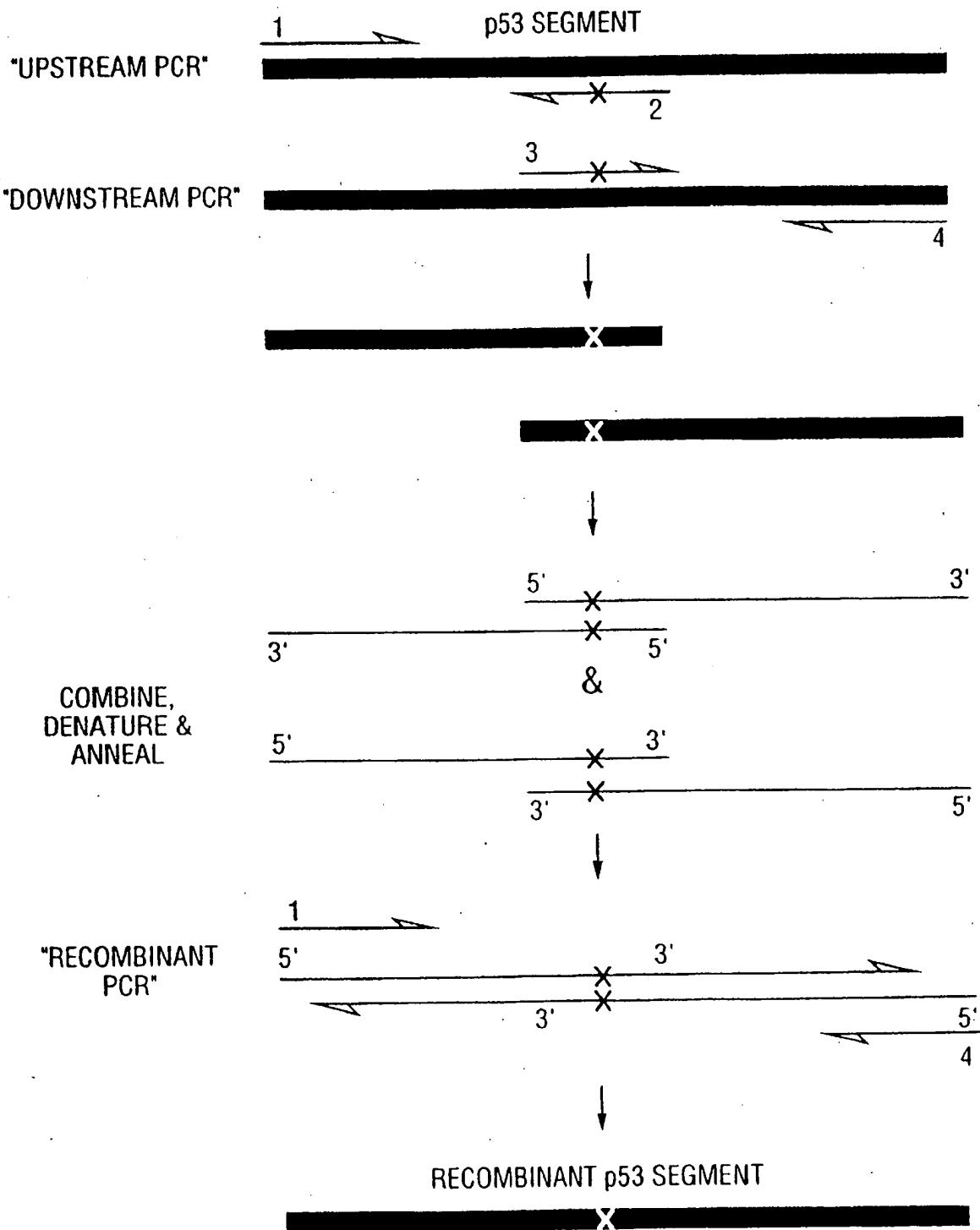
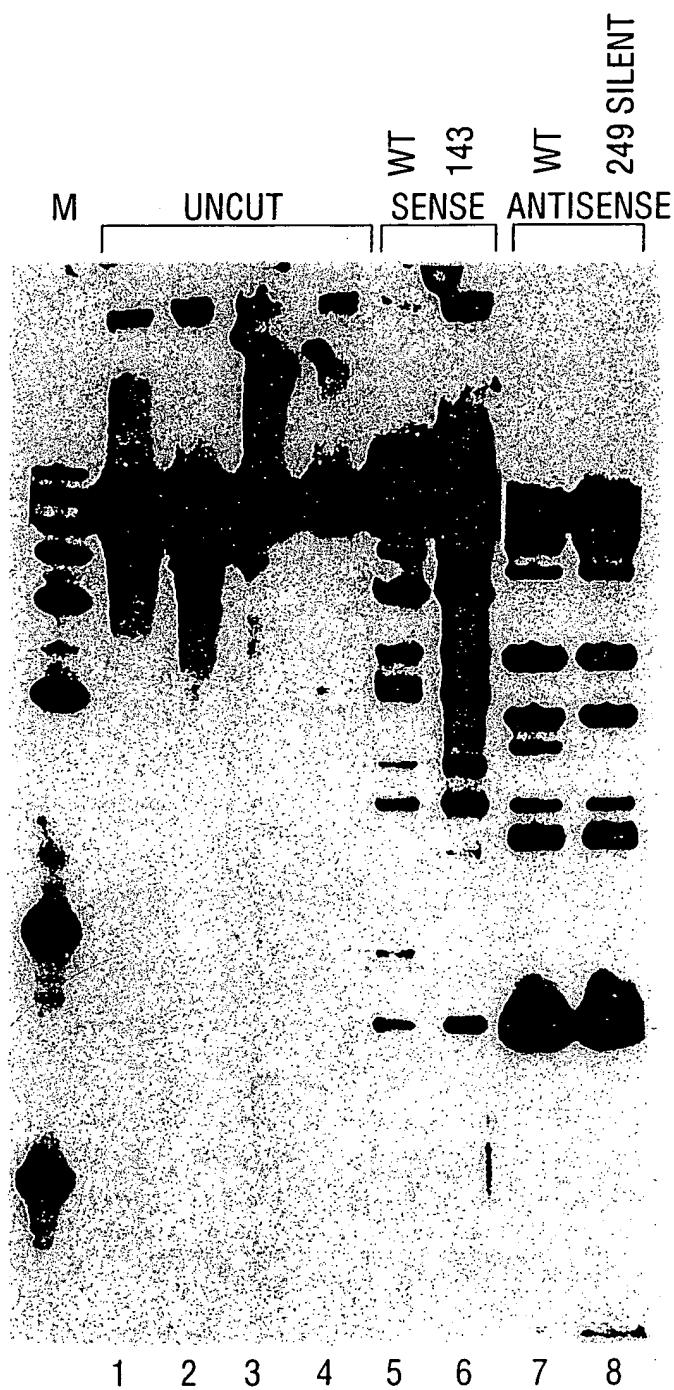


FIG. 77



**FIG. 78**



**FIG. 79**

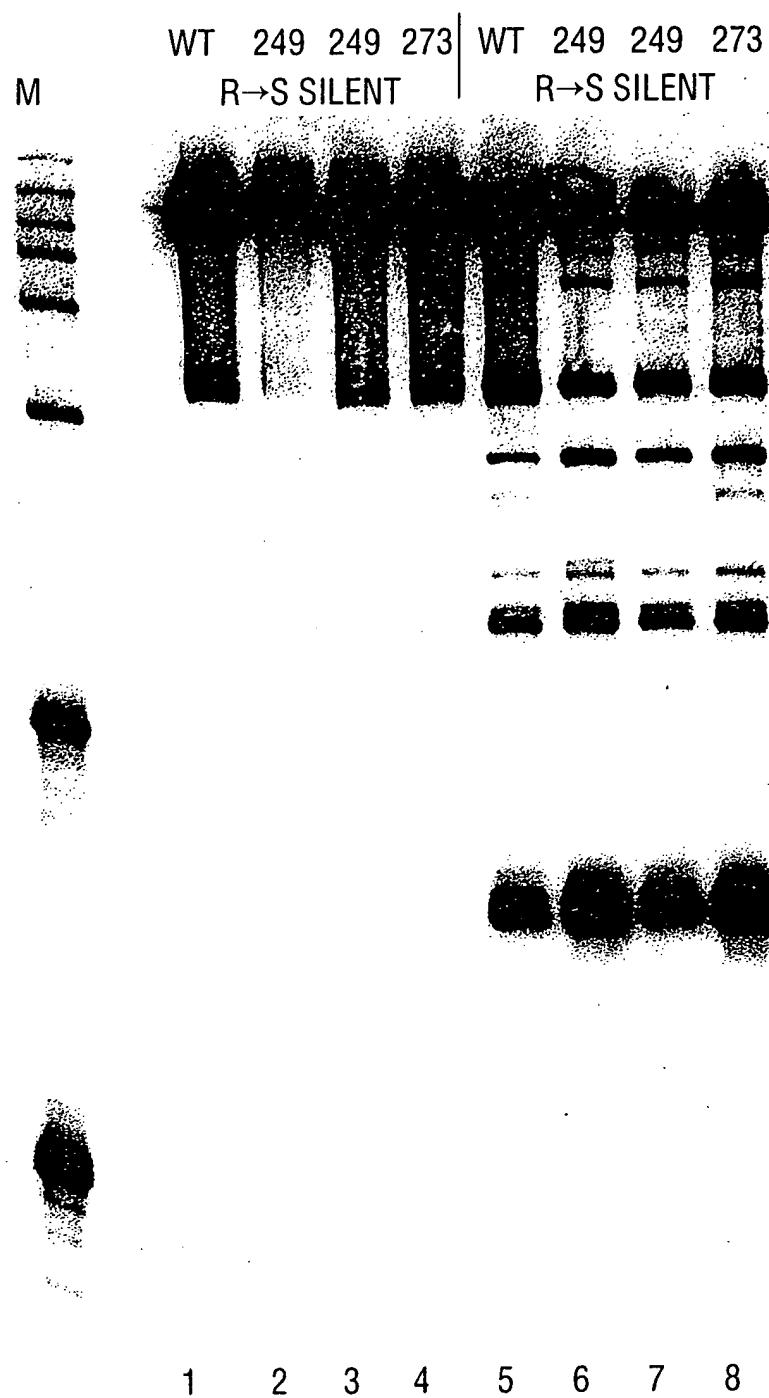


FIG. 80

MIXING PROPORTIONS

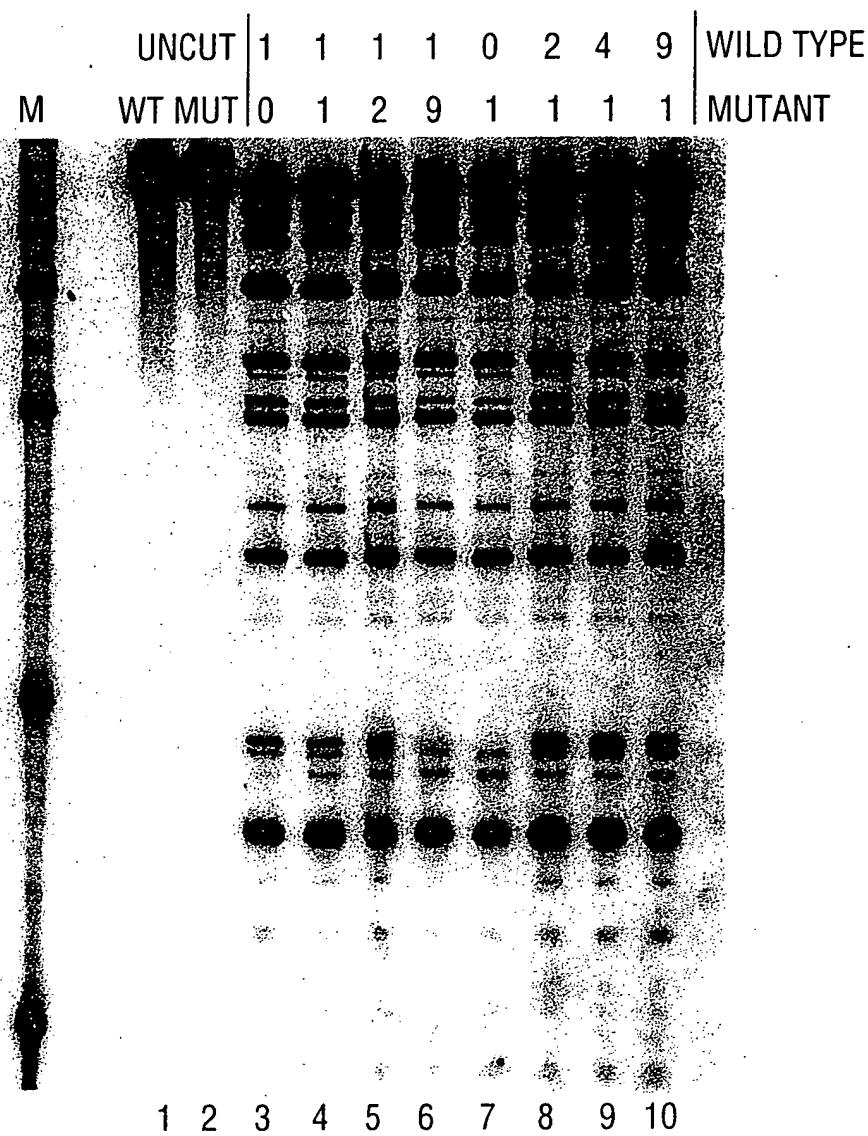


FIG. 81

FIG. 82

1	CTGTCTTCAAC	GCAGGAAAGCG	TCTGGCCATG	GCGTTAGTAT	GAGTGTCTGTG	50
HCV1.1	(SEQ ID NO:121)					
HCV2.1	(SEQ ID NO:122)					
-HCV3.1	(SEQ ID NO:123)					
HCV4.2	(SEQ ID NO:124)					
HCV6.1	(SEQ ID NO:125)					
HCV7.1	(SEQ ID NO:126)					
HCV1.1						
HCV2.1						
HCV3.1						
HCV4.2						
HCV6.1						
HCV7.1						
51	CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGT	CTGCCGAACC	
	CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGT	CTGCCGAACC	
	CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGT	CTGCCGAACC	
	CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGT	CTGCCGAACC	
	CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGT	CTGCCGAACC	
	CAGCCTCCAG	GACCCCCCT	CCGGGAGAG	CCATAGTGT	CTGCCGAACC	
101	GGTGAGTACA	CCGGAATTGC	CAGGAGCACC	GGGTCTTTC	TGGAT- <u>AAA</u>	100
	GGTGAGTACA	CCGGAATTGC	CAGGAGCACC	GGGTCTTTC	TGGAT- <u>CAA</u>	
	GGTGAGTACA	CCGGAATTGC	CAGGAGCACC	GGGTCTTTC	TGGAT- <u>CAA</u>	
	GGTGAGTACA	CCGGAATTGC	CAGGAGCACC	GGGTCTTTC	<u>GGGATGTA</u>	
	GGTGAGTACA	CCGGAATTGC	CAGGAGCACC	GGGTCTTTC	<u>GGGTCTTTC</u>	
	GGTGAGTACA	CCGGAATTGC	CAGGAGCACC	GGGTCTTTC	<u>TGGAT-AAA</u>	
151	CCCGCTCAAT	GCCTGGAGAT	TTGGGGGTGC	CCCCGCAAGA	CTGCTAGCCG	
	CCCGCTCAAT	GCCTGGAGAT	TTGGGGGTGC	CCCCGCAAGA	CTGCTAGCCG	
	CCCGCTCAAT	GCCTGGAGAT	TTGGGGGTGC	CCCCGCAAGA	CTGCTAGCCG	
	CCCGCTCAAT	GCCTGGAGAT	TTGGGGGTGC	CCCCGCAAGA	CTGCTAGCCG	
	CCCGCTCAAT	GCCTGGAGAT	TTGGGGGTGC	CCCCGCAAGA	CTGCTAGCCG	
	CCCGCTCAAT	GCCTGGAGAT	TTGGGGGTGC	CCCCGCAAGA	CTGCTAGCCG	
201	AGTAGTGTG	GGTCGCAGA	GGCTTGTGG	TACTGCTGA	TAGGGTGCCT	200
	AGTAGTGTG	GGTCGCAGA	GGCTTGTGG	TACTGCTGA	TAGGGTGCCT	
	AGTAGTGTG	GGTCGCAGA	GGCTTGTGG	TACTGCTGA	TAGGGTGCCT	
	AGTAGTGTG	GGTCGCAGA	GGCTTGTGG	TACTGCTGA	TAGGGTGCCT	
	AGTAGTGTG	GGTCGCAGA	GGCTTGTGG	TACTGCTGA	TAGGGTGCCT	
	AGTAGTGTG	GGTCGCAGA	GGCTTGTGG	TACTGCTGA	TAGGGTGCCT	
251	GCGAGTGC	GGGGAGGTCT	CGTAGACCGT	GC	282	
	GCGAGTGC	GGGGAGGTCT	CGTAGACCGT	GC		
	GCGAGTGC	GGGGAGGTCT	CGTAGACCGT	GC		
	GCGAGTAC	GGGGAGGTCT	CGTAGACCGT	GC		
	GCGAGTGC	GGGGAGGTCT	CGTAGACCGT	GC		

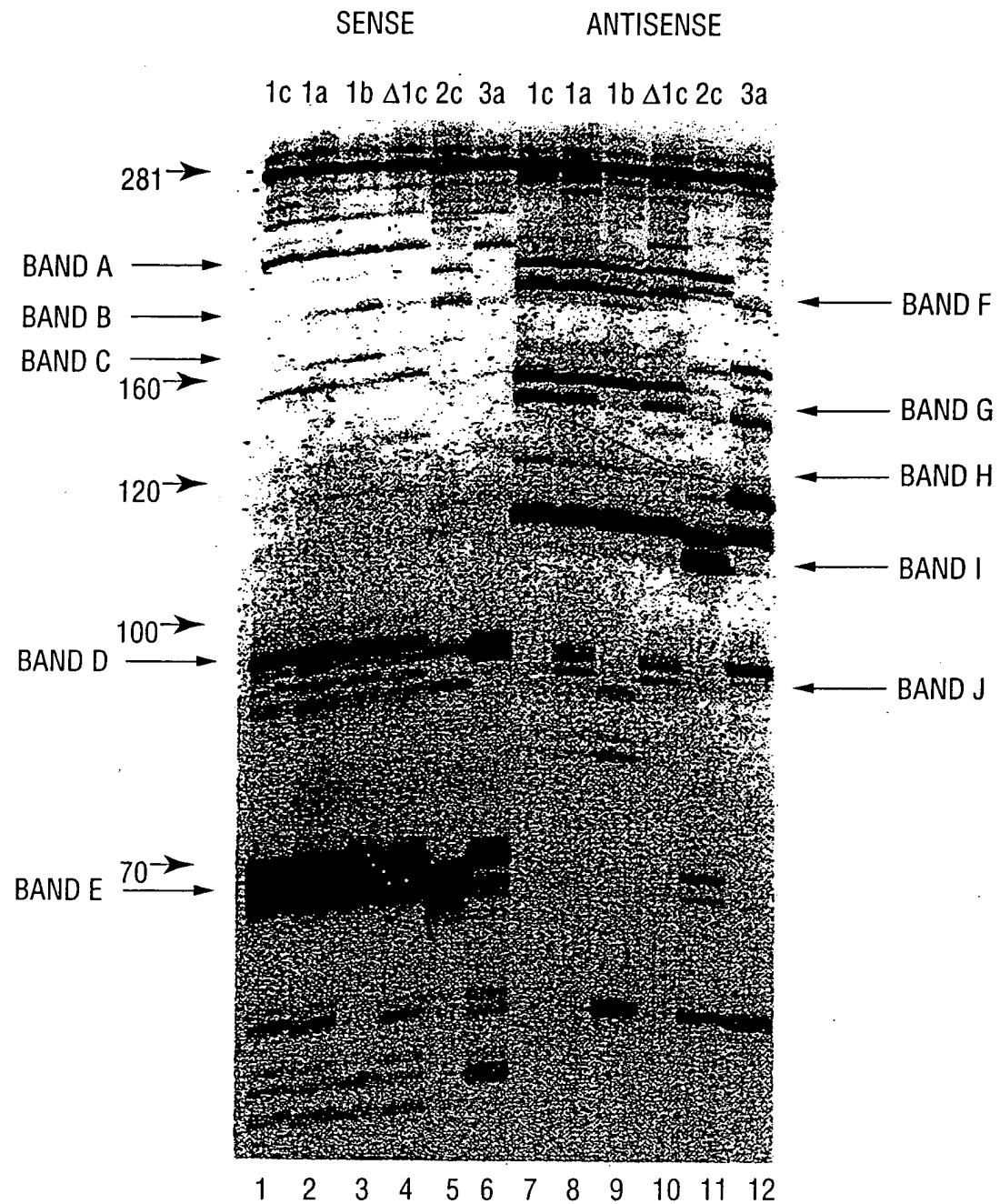


FIG. 83

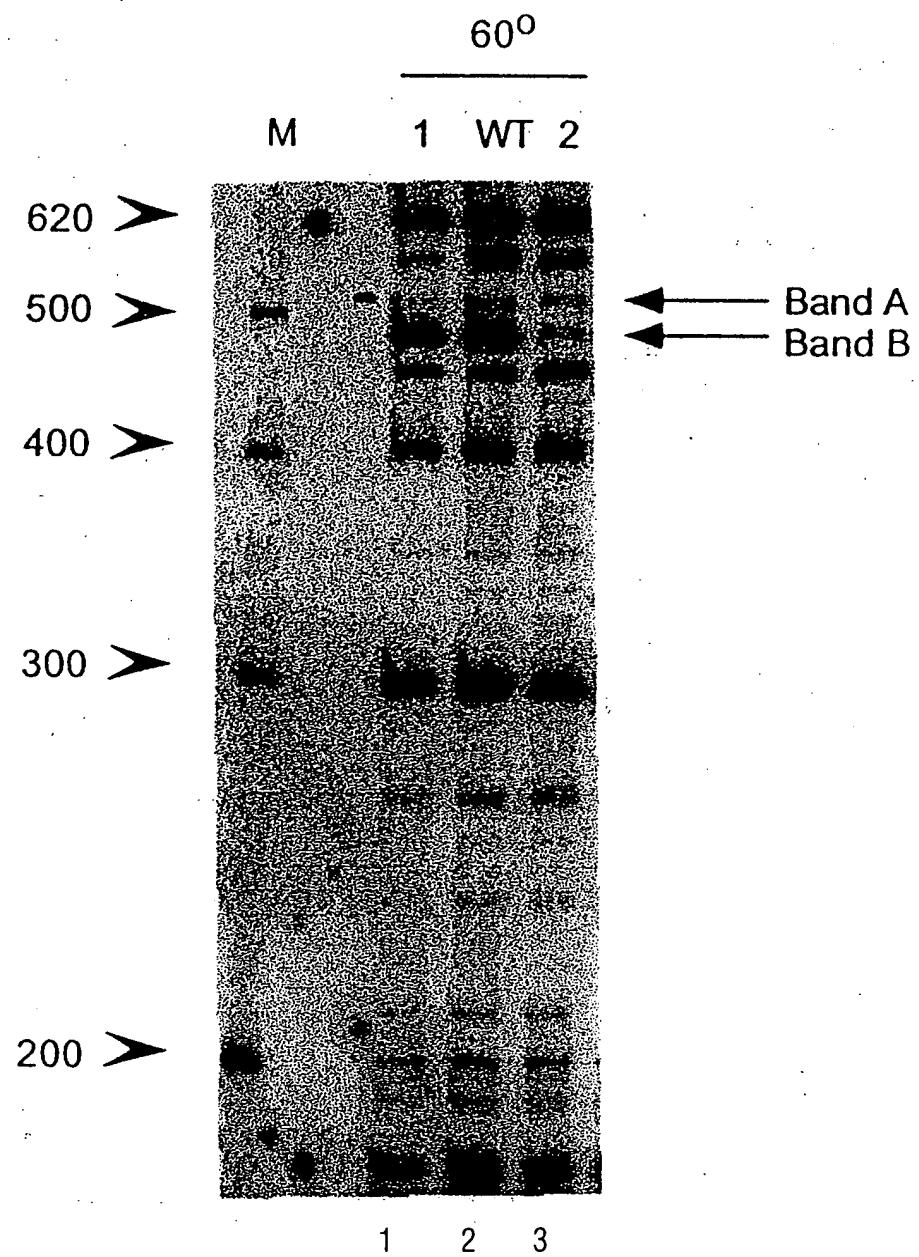


FIG. 84

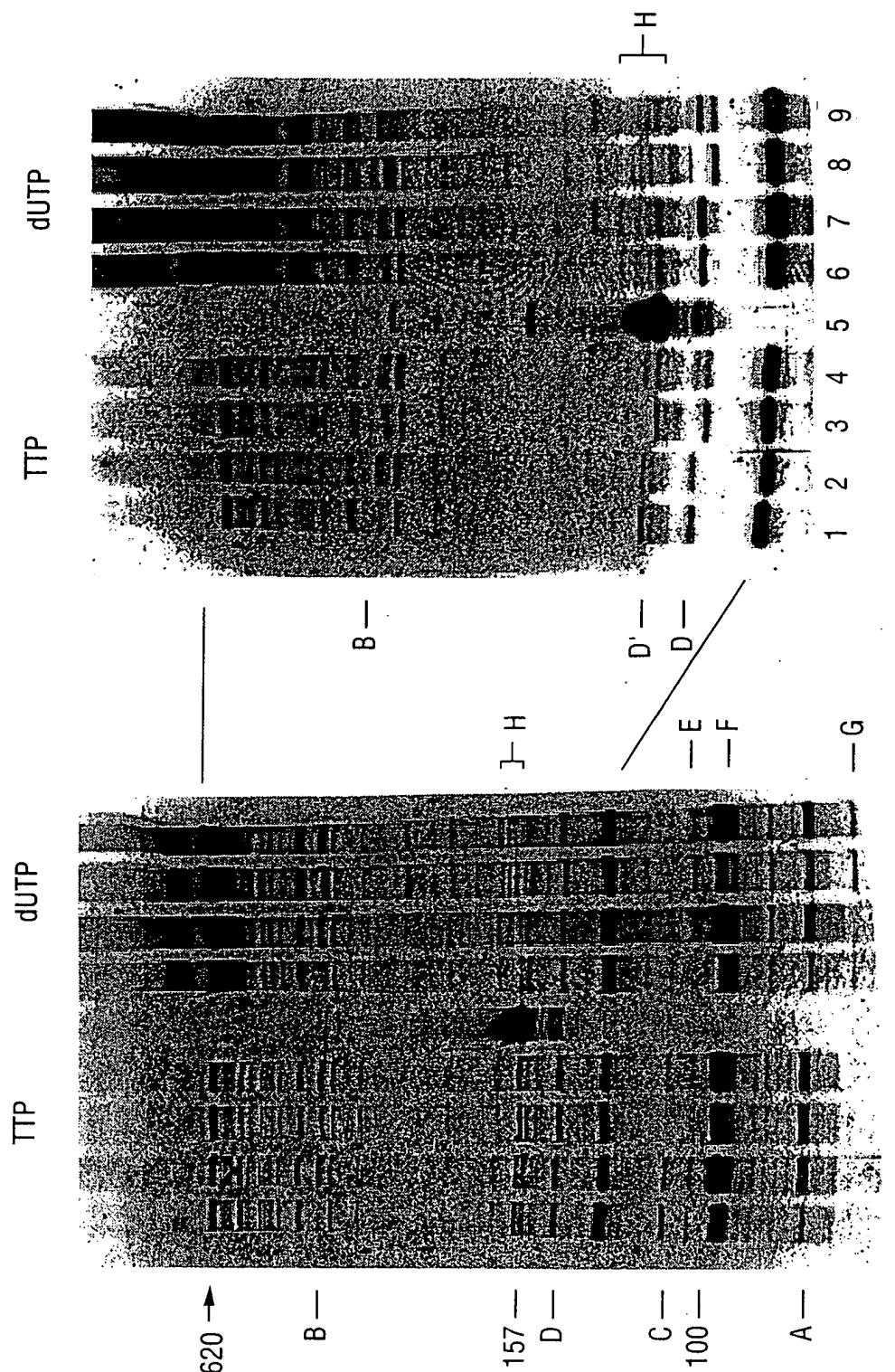


FIG. 85A

FIG. 85B

SENSE STRAND

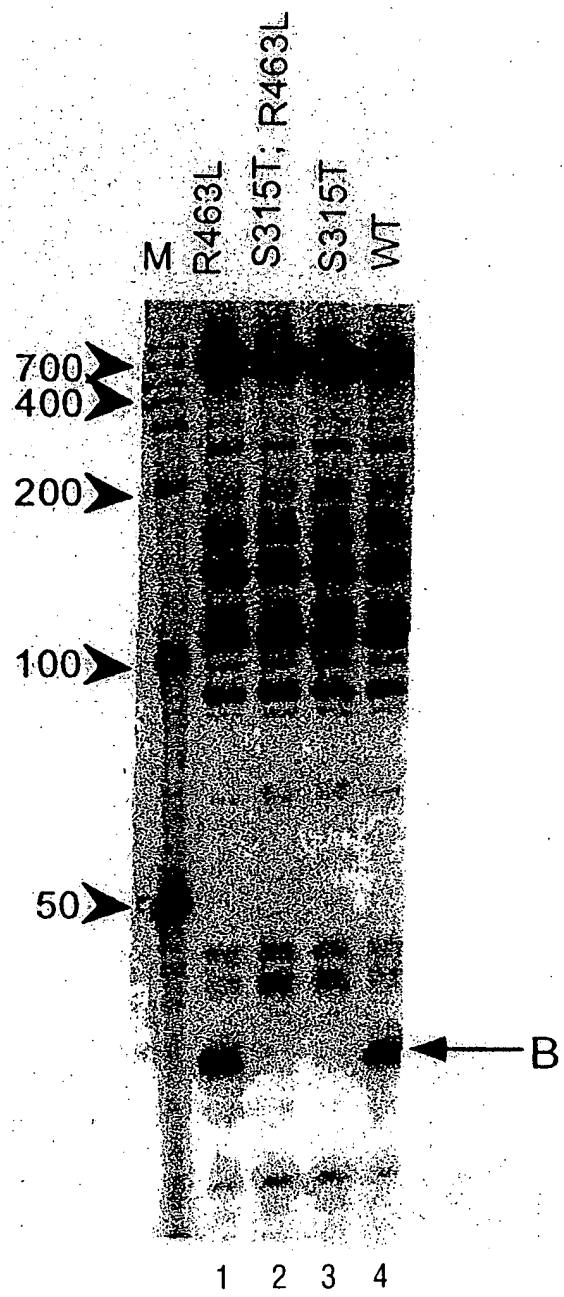
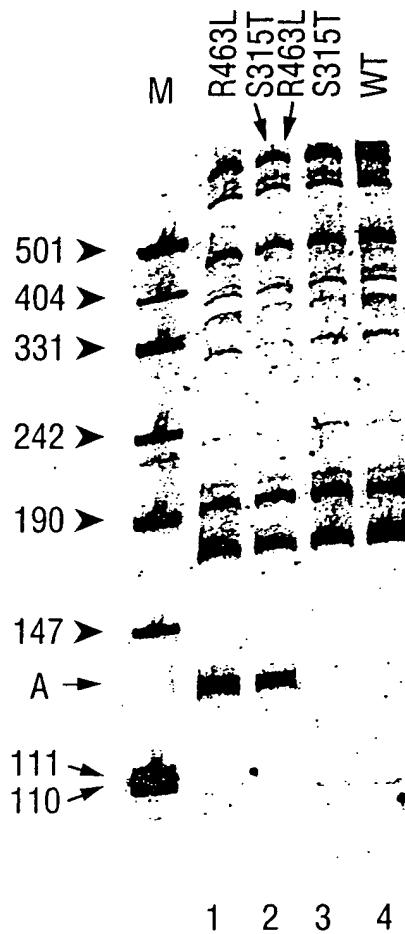


FIG. 86

ANTISENSE STRAND



**FIG. 87**

10	20	30	40	50	60	
AGA	GT <del>TTGATC</del> <sup>T</sup> CT	GGCTCAG				1638
AAATTGAAGA	<u>GT<del>TTGATC</del><sup>T</sup>CT</u> <del>AG</del> <sup>T</sup> AT	GAACGCTGCC	GGCAGGCCTA	ACACATGCAA		
TTAAC <del>TT</del> CT	CAA <del>ACTAG</del> TA	CCGAGTCTAA	CTTGCGACCG	CCGTC <del>CG</del> GT	TGTGTACGTT	
70	80	90	100	110	120	
GTCGAACGGT	AACAGGAAGA	AGCTTGCTTC	TTTGCTGACG	AGTGGCGGAC	GGGTGAGTAA	
CAGCTTGCCA	TTGTCCTTCT	TCGAACGAAG	AAACGACTGC	TCACCGCCTG	GGGIGAGIAA	ER10
130	140	150	160	170	180	
TGTCTGGGAA	ACTGCCTGAT	GGAGGGGGAT	AACTACTGGA	AACGGTAGCT	AATACCGCAT	
ACAGACCCCTT	TGACGGACTA	CCTCCCCCTA	TTGATGACCT	TTGCCATCGA	TTATGGCGTA	
190	200	210	220	230	240	
AACGTCGCAA	GACCAAAGAG	GGGGACCTTC	GGGCCTCTTG	CCATCGGATG	TGCCAGATG	
TTGCAGCGTT	CTGGTTCTC	CCCCTGGAAG	CCCCGAGAAC	GGTAGCCTAC	ACGGGTCTAC	
250	260	270	280	290	300	
GGATTAGCTA	GTAGGGGG	TAACGGCTCA	CCTAGGGGAC	GATCCCTAGC	TGGTCTGAGA	
CCTAA <del>T</del> CGAT	CATCCACCCC	ATTGCCGAGT	GGATCCGCTG	CTAGGGATCG	ACCAAGACTCT	
310	320	330	340	350	360	
GGATGACCAAG	CCACACTGGA	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTGG	
CCTAAC <del>T</del> GGTC	GGTGTGACCT	TGACTCTGTG	CCAGGTC <del>T</del> GA	GGATGGCCCTC	CGTCGTCACC	

FIG. 88A

370	380	390	400	410	420
GGAATTTGC	ACAATGGGG	CAAGCCTGAT	GCAGCCATGC	CGCGTGTATG	AAGAAGGCCT
CCTTATAACG					
TGTTACCCGC					
430	440	450	460	470	480
TCGGGTTGTA	AAGTACTTTC	AGCGGGGAGG	AAGGGAGTAA	AGTTAATACC	TTTGCTCATT
AGCCCAACAT	TTCATGAAAG	TCGCCCCCTCC	TCCTCATT	TCAATTATGG	AAACGAGTAA
490	500	510	520	530	540
GACGTTACCC	GCAGGAAGAAG	CACCGGCTAA	CTCCCGTGCCTA	GCAGGCCGGG	TAATACGGAG
CTGCAATGGG					
550	560	570	580	590	600
GGTGCAGCG	TTAATCGGAA	TTACTGGGG	TAAGCCAC	GCAGGGCGTT	TGTTAAGTCA
CCACGGTCCG	AATTAGCCTT	AATGACCCGC	ATTCGGCGTG	CGTCCGCCAA	ACAATTCACT
610	620	630	640	650	660
GATGTGAAT	CCCCGGGCTC	AACCTGGGAA	CTGCATCTGA	TACTGGCAAG	CTTGAGTCTC
CTACACTTA	GGGGCCCGAG	TTGGACCCCT	GACGTAGACT	ATGACCGTTC	GAACTCAGAG
670	680	690	700	710	720
GTAGAGGGGG	GTAGAATTCC	AGGTGTAGCG	GTGAATGCG	TAGAGATCTC	GAGGAATACC
CATCTCCCCC	CATCTTAAGG	TCCACATCGC	CACTTACGC	ATCTCTAGAC	CTCCTTATGG
730	740	750	760	770	780
GGTGGCGAAG	GCGGCCCCCT	GGACGAAGAC	TGACCGCTCAG	GTGCGAAAGC	GTGGGGAGCA
CCACCGCTTC	CGCGGGGGA	CCTGCTTCTG	ACTGCGAGTC	CACGCTTTCG	CACCCCTCGT

**FIG. 88B**

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FIG. 88C

1210	1220	1230	1240	1250	1260
ATCATGGCC	TTA				
ATCATGGCC	TTACGA				
<u>ATCATGGCC</u>	<u>TTACG</u> <u>ACCAG</u>	<u>GGCTACACAC</u>	<u>GTGCTACA</u>	<u>GGCGCATACA</u>	<u>AAGAGAAGCG</u>
TAGTACCGG	AATGCTGGTC	CCGATGTGTG	CACGATGTTA	CCGGTATGT	TTCTCTCGC
1270	1280	1290	1300	1310	1320
ACCTCGCGAG	AGCAAGCGGA	CCTCATAAAG	TGCGTCGTAG	TCCGGATTGG	AGTCTGCAAC
TGGAGCGCTC	TCGTTCGCCT	GGAGTATTTC	ACGCAGCATC	AGGCCTAAC	TCAGACGTTG
1330	1340	1350	1360	1370	1380
TCGACTCCAT	GAAGTCCGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATACGT
AGCTGAGGTA	CTTCAGCCTT	AGCGATCATT	AGCACCTAGT	CTTACGGTGC	<u>CACTTATGCA</u>
			GC	CACTTATGCA	
1390	1400	1410	1420	1430	1440
TCCCGGGCT	TGTACACACC	GCCCCGTCA	CCATGGGGAGT	GGGTTGCAA	AGAAGTAGGT
<u>AGGGCCCGGA</u>	<u>ACATGTGTGG</u>	<u>CGGGCAGTGT</u>	<u>GGTACCCCTCA</u>	<u>CCCAAACGTTT</u>	<u>TCTTCATCCA</u>
AGGGCCCGGA	ACATG				
1450	1460	1470	1480	1490	1500
AGCTTAACCT	TCGGGAGGGC	GCTTACCACT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA
TCGAATTGGA	AGCCCTCCCC	CGAATGGTGA	AACACTAAGT	ACTGACCCCC	CTTCAGCATT
1510	1520	1530	1540	1550	
CAAGGTTAAC	GTAGGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA.....	
GTTCCATTGG	CATCCCCCTTG	GACGCCAAC	TAGTGGAGGA	AT.....	

SB-3  
SB-4

**FIG. 88D**

1638 (SEQ ID NO:151) AGAGTTGATCCTGGCTCAG  
 E.colirrSE (SEQ ID NO:158) 0 ..AAATTGAAAGAGTTGATCAGGCTCAGATTGAACCGCTGGGGCAGGCCAACATGCA  
 Cam.jejuns (SEQ ID NO:159) 0 ..TTTTATGGAGTTGATCCTGGCTCAGAGTGAAGCTGGGGGTCATAATACATGCA  
 Stp.aureus (SEQ ID NO:160) 0 ..TTTTATGGAGTTGATCCTGGCTCAGGATGAACGCCAGCTGGGGCTGCA  
 ER10 (SEQ ID NO:152) 60 AGTCGAAACGGTAACAG-----GAAGAACGTTGCTTCTT-----GCTGACGAGTGGGGGACGGG  
 E.colirrSE 62 AGTCGAAACGGAT-----GAAGCTCTAGCTGCTAGAGTGG-----TTAGTGGGGCACGGG  
 Cam.jejuns 61 AGTCGAGCGAA-----CGGACGAGAAGCTGCTCTGATG-----TT-AGGGGGACGGG  
 Stp.aureus  
 ER10  
 E.colirrSE  
 Cam.jejuns  
 Stp.aureus  
 114 TGAGTAATGCTGGGA-ACTGCCTGATGGAGGGGATAACTACTGGAAACGGTAGCTAATA  
 114 TGAGTAAGGTATAGTTAACCTGCCCCAACAGAGGACAAACAGTTGAAACGACTGCTAATA  
 113 TGAGTAACACGGTGGATAACCTACCTATAAGACTGGATAACTTGGAAACCGGAGCTAATA  
 175 CCGCATAAC-----GTCGCAAGAC-----CAAAGAGGGGACCTTCG-GGCGCTCTG  
 176 CTCTTAACTCTCTGCTAACACAAGTGGTAGG-GAAAG-----TTTT-----CG  
 175 CCGGATAATATTTGAACCGCATGGTCAAAGTGAAGACGGGT-----CTT-----GCTGTCA  
 221 CCATGGGATGTGCCAGATGGGATTAGCTAGTAGGTGGGTAACGGCTCACCTAGGGACGA  
 221 GTGTAGGGATGAGACTATAGTATCAGCTAGTTGGTAAGGTAATGGCTTACCAAGGGTATGA  
 229 CTTATAGATGGATCCGGCCTGCATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGA  
 283 TCCCTAGCTGGTCTGAGAGGGATGACCCACACTGGAACTGAGACACGGTCCAGACTCCTA  
 283 CGCTTAACCTGGTCTGAGAGGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGACTCCTA  
 291 TACGTAAGCCGACCTGAGAGGGTGATCGGCCACACTGGAACTGAGACACGGTCCAGACTCCTA  
 ACTCCTA  
 1659 (COMPL)

FIG. 89A

E.coli rrSE  
Cam.jejun5  
Stp.aureus  
1659 (COMPL)

345 CGGGAGGCAGCTGGGAATTTGACAAATGGGCCAAGCCTGATGCCAGCCATGCCCGCTG  
345 CGGGAGGCAGCTGGGAATTTGACAAATGGGCCAAGCCTGATGCCAGCCACGCCCGCTG  
353 CGGGAGGCAGCTGGGAATTTGACAAACGCCCTGACGCCAGCAACGCCCGCTG  
CGGGAGGCAGCAG

E.coli rrSE  
Cam.jejun5  
Stp.aureus

407 TATGAAAGAAGGCCTTCGGGTGTAAAGTACTTCAGCGGGAGGA-GGGACTAAAGTAA  
407 GAGGATGACACTTTGGAGCGTAACCTCTTCTTAGGGAAAG-----AATT  
415 AGTGATGAAGGTCTCGGATCGTAAACTCTGTATTAGGGAAAGAACATATGTGTAAGTAAC

E.coli rrSE  
Cam.jejun5  
Stp.aureus

468 ACCTTTGCTCATTGACGTTACCCGAGAAGAACCGGCTAACTCCGTGCCAGGCCCG  
455 C-----TGACGGTACCTAAGGAATAAGCACCGGCTAACTCCGTGCCAGGCCCG  
476 -----TGTCACATCTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGGCCCG

FIG. 89B

"Replacement Sheet"

E. coli rrSE	530	GTAATACGGAGGGTGC
Cam. jejun5	506	GTAATACGGAGGGTGC
Stp. aureus	538	GTAA
		TAACGGTGGCAAGCGT
		ATTCCGGAAATTGGCGT
		AAAGCGCGTAGGGGTT
E. coli rrSE	592	GTTAAGTCAGATGTGA
Cam. jejun5	568	ATCAAGTCTTGTGA
Stp. aureus	600	AA
		TTAAGTCTGATGTGA
		AAAGCCCACGGCTAAC
		CGTGGAGGGTCATTGGA
		AAACTGGAAACTGGAAAC
E. coli rrSE	654	GAGTCTCGTAGAGGGGG
Cam. jejun5	630	TAGAATTCCAGGTAGCG
Stp. aureus	662	GA
		GAGTGGAGGAGAGGCAGA
		TGGAATTGGTGTAGGGG
		TAATCCGTAGATATCACC
		AGA
E. coli rrSE	716	ATACCGGTGGCGAAGGG
Cam. jejun5	692	CCCCCTGGACGAAGACT
Stp. aureus	724	GGACGCTCAGGTGGAAAG
		CGCTGGGAAGCGCTGGGA
		CAACTGACGCTAAGGCCG
		AAAGCGCTGGGA
		ACACCAAGTGGCGAACCTT
		CTGGTCTGTAACTGACG
		CTGTGTAAGTGTGGAAAG
		CGCTGGGA
E. coli rrSE	778	GCAACAGGATTAGATAC
Cam. jejun5	754	CCCTGGTAGCCACGCC
Stp. aureus	786	TAACCGATACCC
		GGTAGTCCACGCCGTAAC
		CGATGAGTGTCAAGTGT
		TTAGGGG

FIG. 89C

"Replacement Sheet"

E. coli rrSE	840	C- <u>CTTGA</u> -GGGTGGCTCCGGAGCTAACGGCTTAAGTCGACCCCTGGGACTACGGCC
Cam. jejun5	816	G- <u>CTAGT</u> -CATCTCACTAATGCAGCTAACGGCTTAAGTGTACCCCTGGGAGTACGGTCGC
Stp. aureus	848	GT- <u>TTCCG</u> CCCTTAGTGCTGCAGCTAACGCATTAAACGCACTCCGCCTGGGAGTACGACCCG
E. coli rrSE	900	AAGGTTAAACTCAAATGAATTGACGGGGCCACAAAGCGGTGGACATGTGGTTAATT
Cam. jejun5	876	AAGGTTAAACTCAAAGGAATAGACGGGGACCCGCACAAAGCGGTGGAGCATGTGGTTAATT
Stp. aureus	909	AAGGTTGAAACTCAAAGGAATTGACGGGGACCCGCACAAAGCGGTGGAGCATGTGGTTAATT
E. coli rrSE	962	CGATGCAACGGCGAACCTTACCTGGTCTTGACATCCACGGAGTTTCAGAGATGAGAAT
Cam. jejun5	938	CGAAGATAGCGGAAGAACCTTACCTGGCTTGTATCTTAAGAACCTTTAGAGATAAGAGG
Stp. aureus	971	CGAAGCAACGCCAACCTTACCAAATCTTGACATCTTGTACAACACTCTAGAGATAGAGCC
E. coli rrSE	1024	GTG- <u>CCTTCGGG</u> -AA=CCGTGAGACAGGTGCTGCATGGCTGTCAGCTCGTGTGTA
Cam. jejun5	1000	GTGCTAGCTTGCTAGAA-CTTAGAGACAGGTGCTGCACGGCTGTGTCAGCTCGTGTGTA
Stp. aureus	1033	TTCC- <u>CCTCGGG</u> -GGACAAAGTGACAGGTGGTGCATGGTTGTCAGCTCGTGTGTA
SB-1		GCACCGAGCCAAACCC
E. coli rrSE	1081	AATGTTGGGTTAACGTCGGCAACGGCGAACCCCTTATCCTTGTGCCCCGGAGCGGTCGG-CC
Cam. jejun5	1061	GATGTTGGGTTAACGTCGGCAACGGAGCGAACCCACGGTATTAGTTGCTAACGGTTGG-CC
Stp. aureus	1092	GATGTTGGGTTAACGTCGGCAACGGAGCGAACCCCTTAAGCTTAGTTGCTAACGTCAGT-TTAAGT-T

FIG. 89D

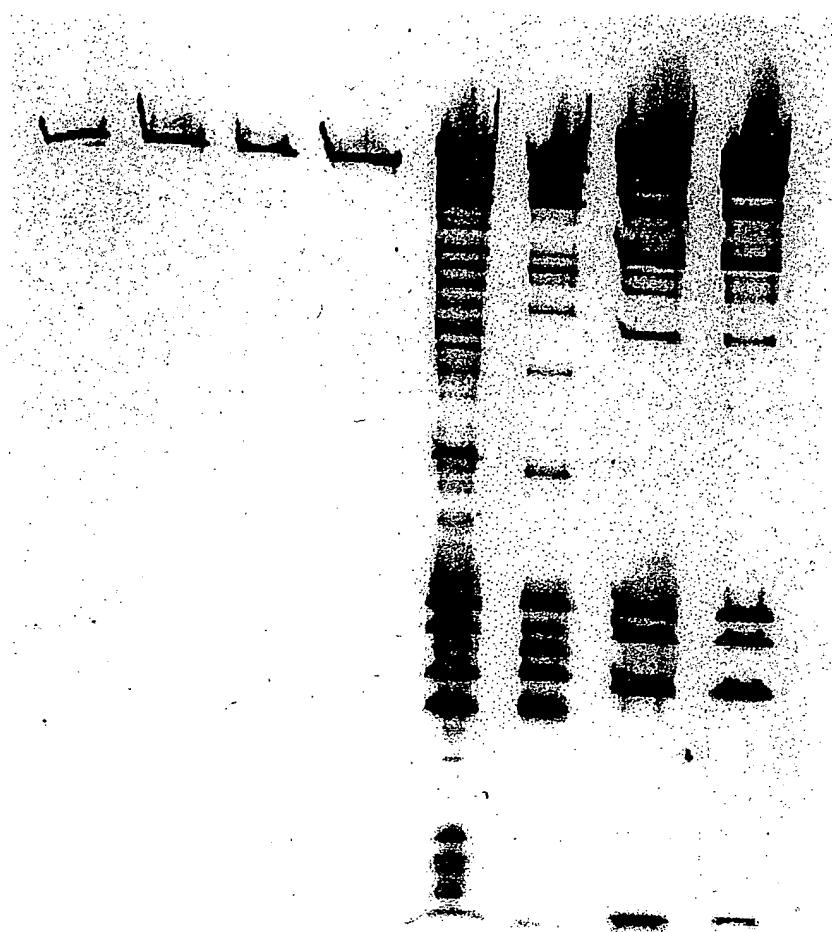
SB-3	(SEQ ID NO:157)	ATGACGTCAGTCATC
SB-4	(SEQ ID NO:154)	ATGACGTCAGTCATC
E.colirrSE	1142 GGGAACTCAAAGGAGACTGGCAGTGATAACTGGAGGAAGGTGGGGATGACGTCAGTCATC	
Cam.jejunS	1122 GAGCACTCTAAATAGACTGCCCTCG-TAAGGAGGAGGAAGGTGGGACGACTCAAGTCATC	
Stp.aureus	1152 GGGCACTCTAAGTGAECTGCCGGTACAACGGAGGAAGGTGGGATGACGTCAGTCATC	
SB-3	ATGGCCCTTA	
SB-4	ATGGCCCTTACGGA	
E.colirrSE	1204 ATGGCCCTTACGACCAGGGCTACACACCGTGTACAATGGCATATAGAATGAGACGCAATTAC	
Cam.jejunS	1183 ATGGCCCTTATGCCAGGGGACACACGTGTACAATGGCATATAGAATGAGACGCAATTAC	
Stp.aureus	1214 ATGGCCCTTATGTTGGCTACACACCGTGTACAATGGACAATACAAGGGAGGGAAACC	
E.colirrSE	1266 GCGAGAGGCAAGCGGACCTCATAAAGTGGCTAGTGGAGTCTGCAACTCGACTC	
Cam.jejunS	1245 GCGAGGCTGGAG-CAATCTATAAAATATGTCCTCAGTTCGGATTCTGCACACTCGAGAG	
Stp.aureus	1276 GCGAGGCTAACGCAAATCCATAAAGTGGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTA	
E.colirrSE	1328 CATGAAGTCGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACCGTGAATACGTTGGGGC	
Cam.jejunS	1306 CATGAAGCCGGAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTGGGGT	
Stp.aureus	1338 CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTGGGGT	
1743 (compl)	CGGTGAATACGTTGGGGC	

FIG. 89E

E. coli rrSE	1389	CTTGTACACCGCCCCGTACACCATGGAGGGTTGCAAAGAAGTAGGTAGCTTAACCT
Cam. jejun5	1368	CTTGTACTCACCGCCCCGTACACCATGGAGTTGATTCACTCGAAGCCGGAATACT <u>-A-A</u>
Stp. aureus	1399	ATTGTACACACCGCCCCGTACACACCAGAGAGTTGTAACACCCGAAGCCGGTGGAGTAACCT
1743 (compl)		CTTGTAC
E. coli rrSE	1451	TCG <u>=</u> GGAGGGCGTTACCACTTGTGATTCACTGGGGTGAAGTAGTCGTAACAAGGTAACCG
Cam. jejun5	1427	AC <u>--</u> T <u>=</u> AGTTACCGTCCACAGTGGATCAGCGACTGGGTGAAGTCGTAACAAGGTAACCG
Stp. aureus	1461	TTTAGGAGCTAGCCGTCGAAGGTGGACAATGATTGGGTGAAGTCGTAACAAGGTAACCT
E. coli rrSE	1512	TAGGGAACCTGGCGGTGGATCACCTCCCTA---
Cam. jejun5	1485	TAGGAGAACCTGGCGGTGGATCACCTCCT---
Stp. aureus	1523	TATCGGAAGGTGGGCTGGATCACCTCTTCT

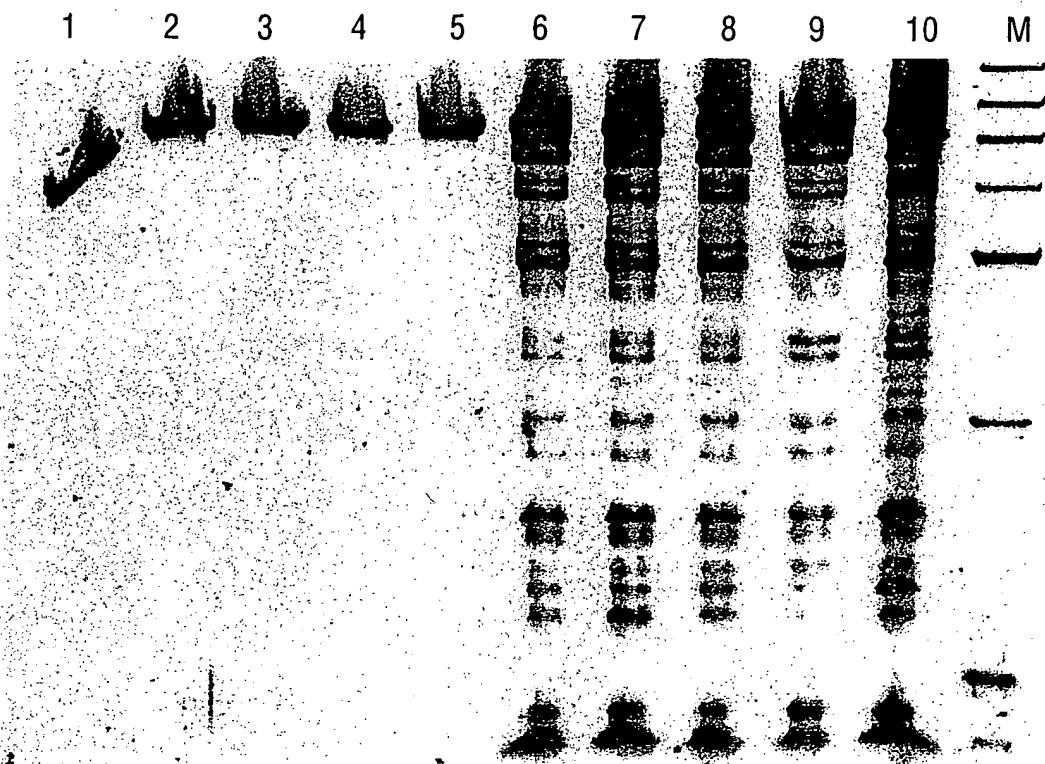
FIG. 89F

1 2 3 4 5 6 7 8

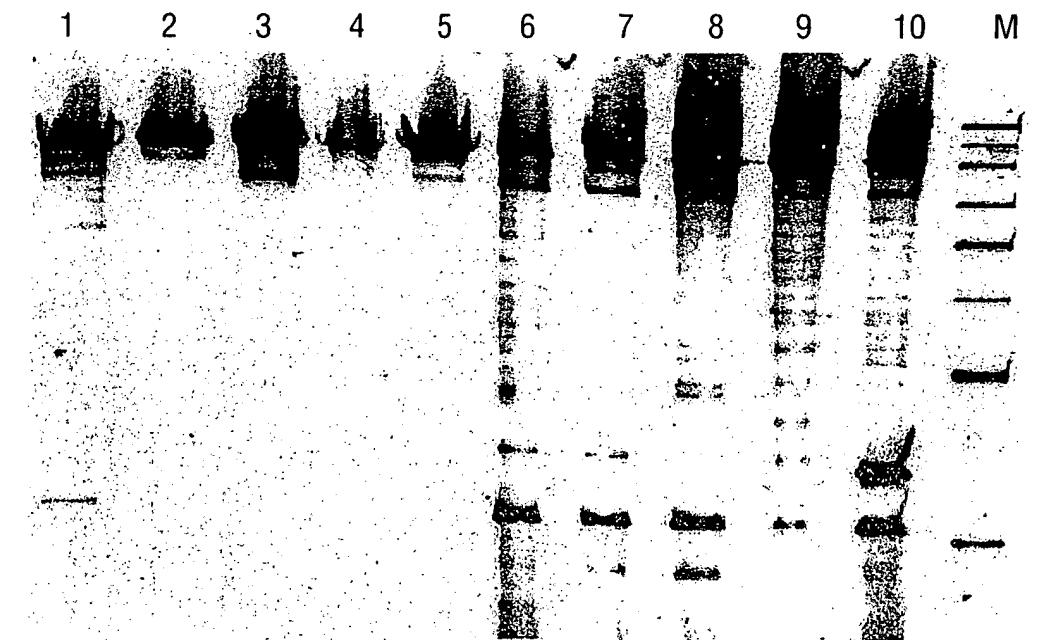


**FIG. 90**

"Replacement Sheet"



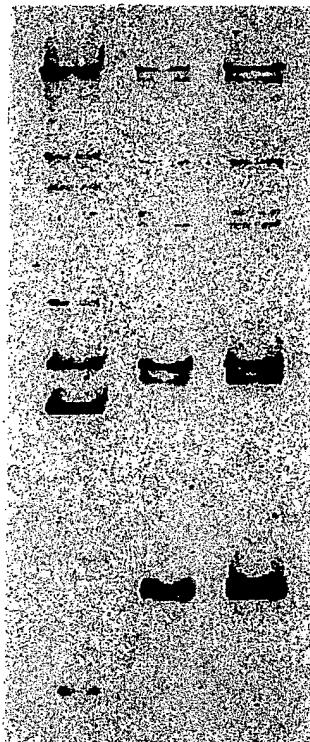
**FIG. 91A**



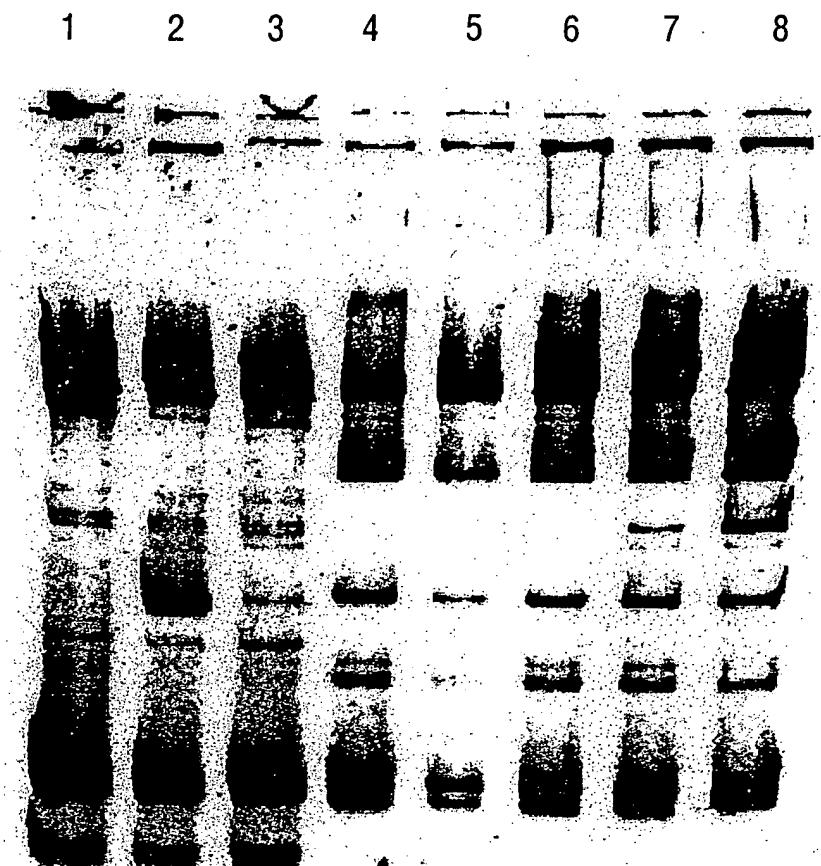
**FIG. 91B**

"Replacement Sheet"

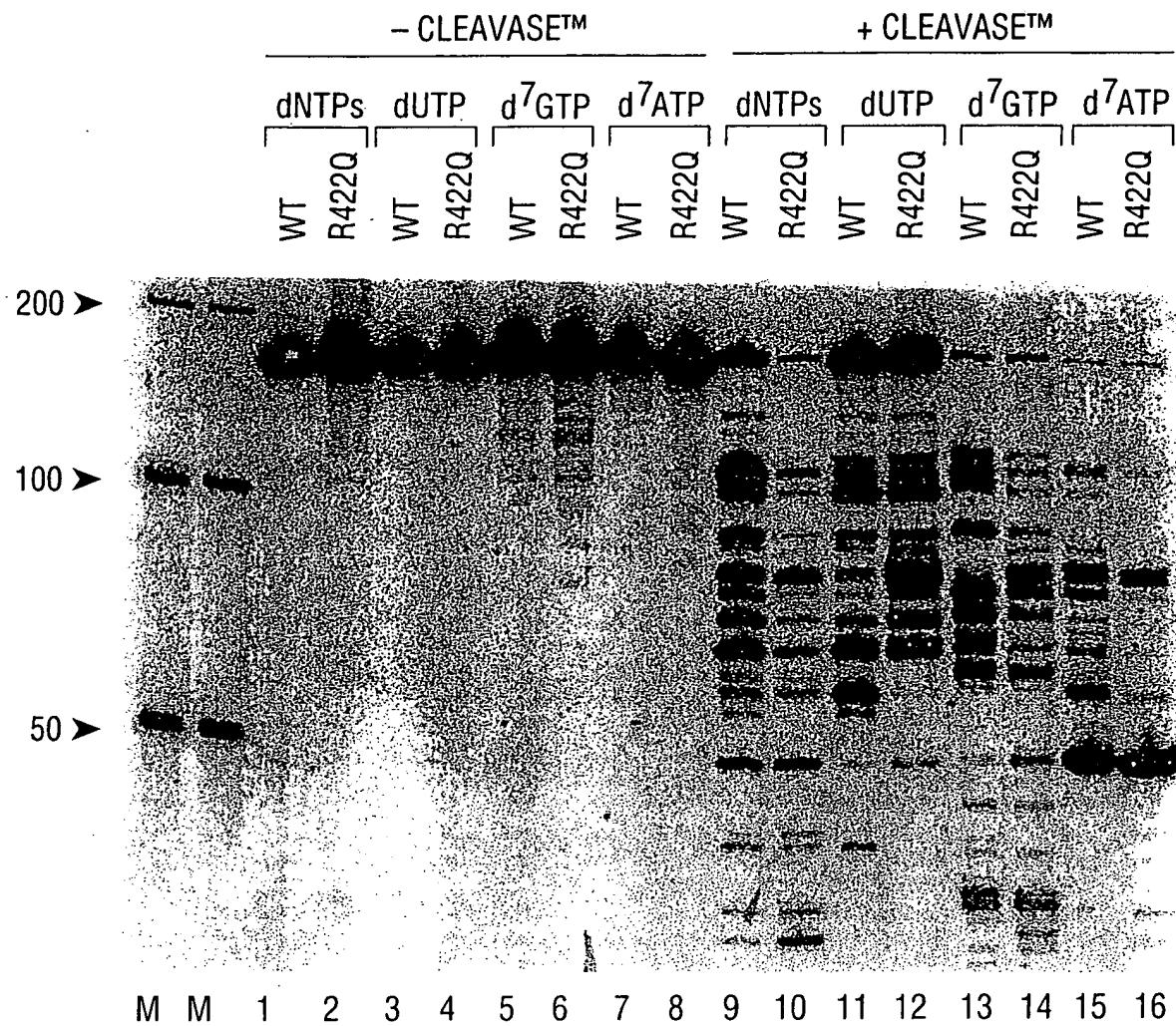
1 2 3



**FIG. 92**



**FIG. 93**



**FIG. 94**

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